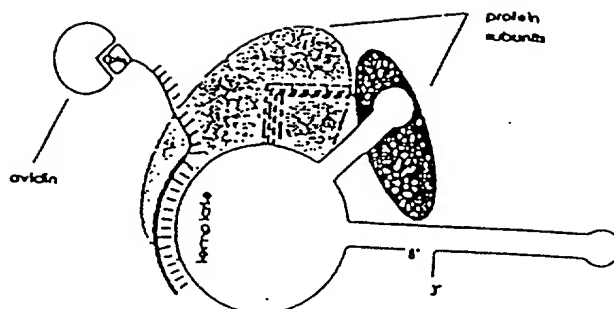


PANEL A



PANEL B

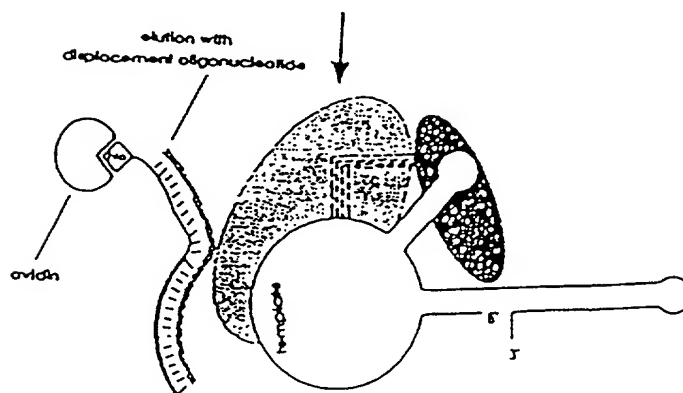


FIGURE 2

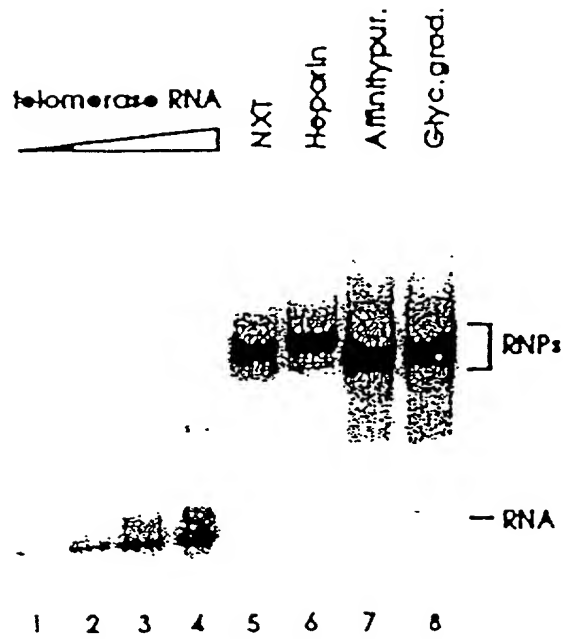
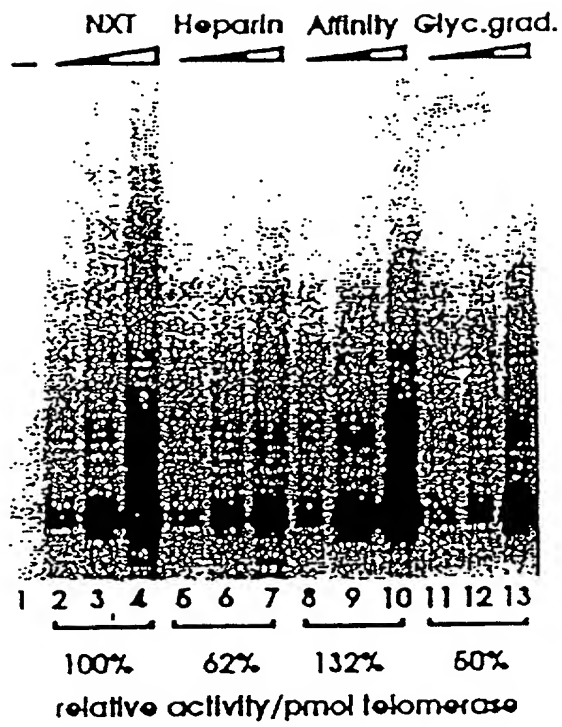


FIGURE 3



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FIGURE 4

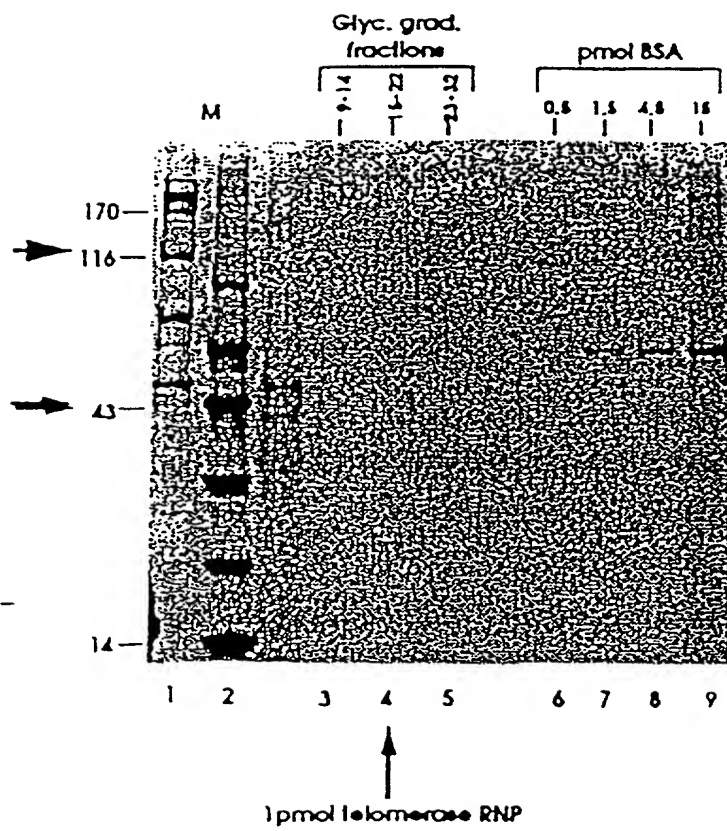


FIGURE 5

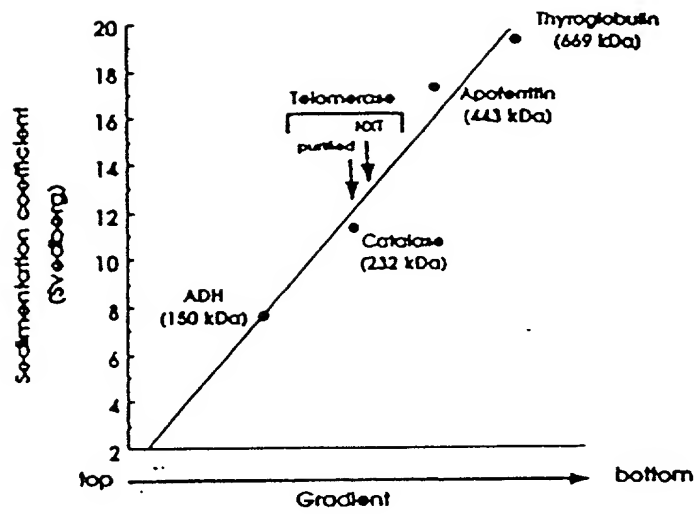


FIGURE 6

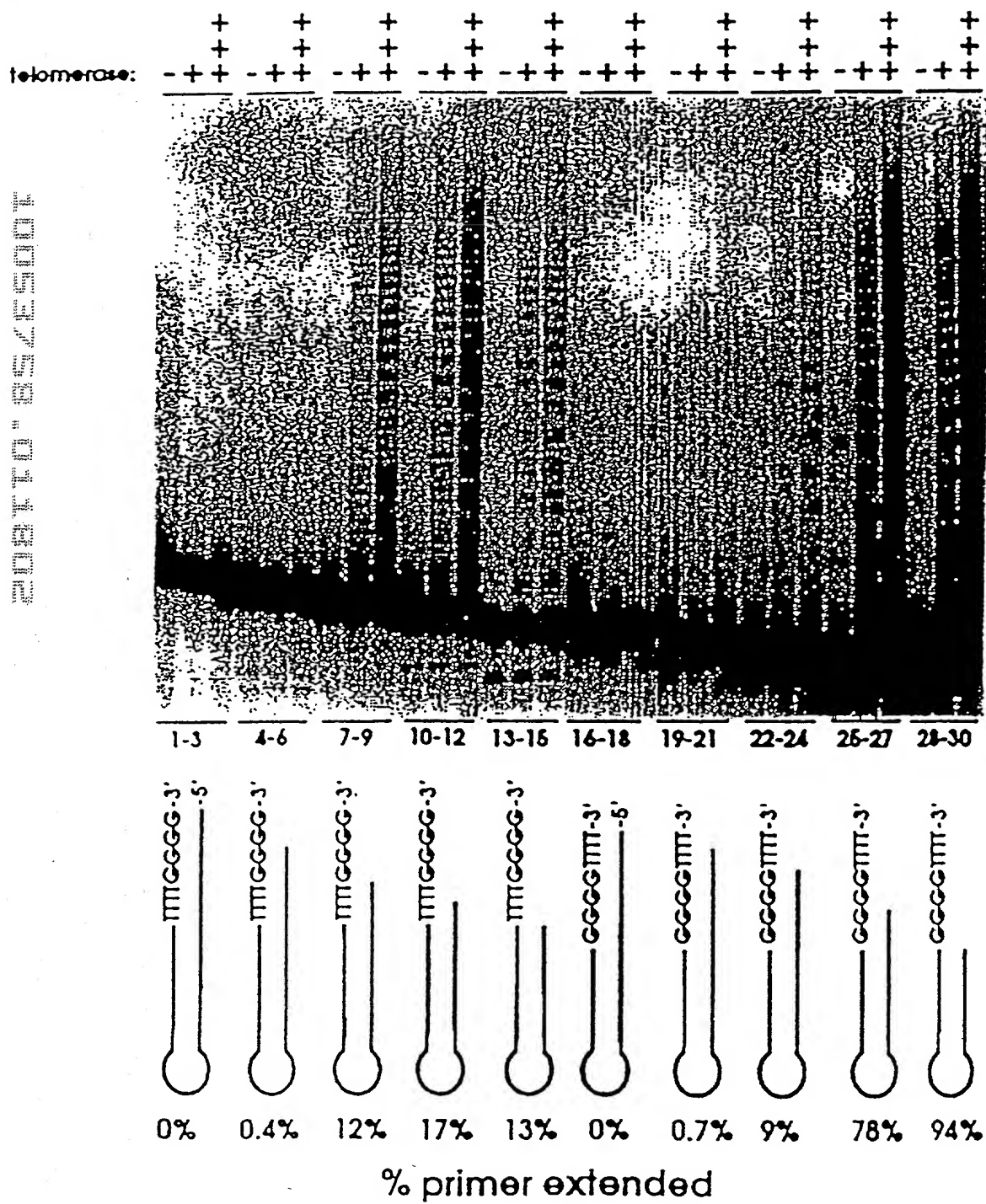


FIGURE 7

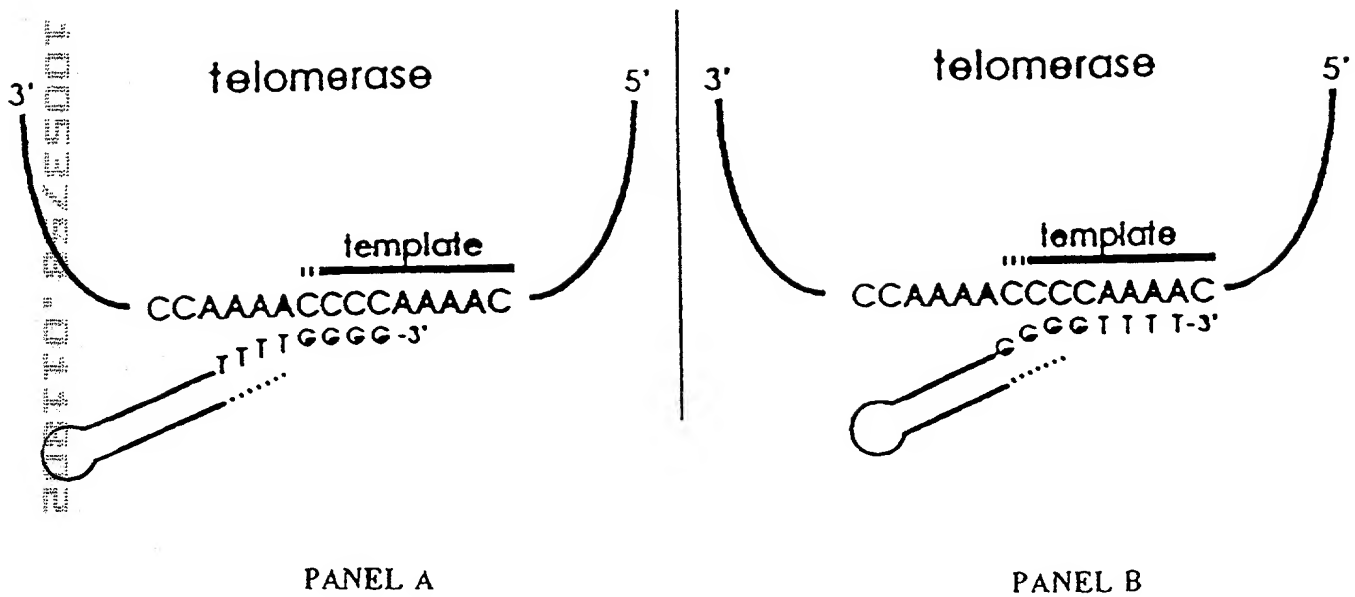
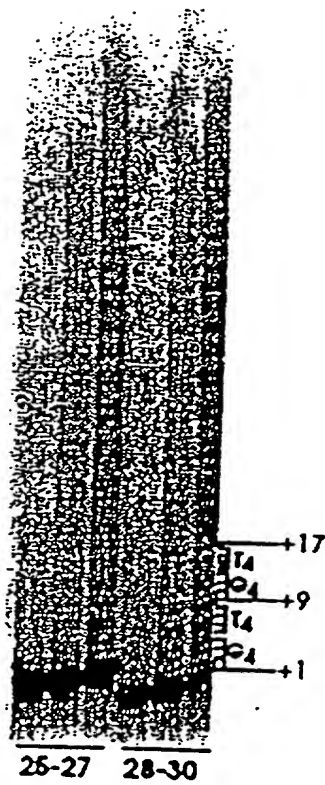


FIGURE 8



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FIGURE 9

1 AAAACCCCAA AACCCCAAAA CCCCTTTTAG AGCCCTGCAG TTGGAAATAT  
51 AACCTCAGTA TTAATAAGCT CAGATTTTAA ATATTAATTA CAAAACCTAA  
101 ATGGAGGTTG ATGTTGATAA TCAAGCTGAT AATCATGGCA TCACTCAGC  
151 TCTTAAGACT TGTGAAGAAA TTAAAGAAGC TAAAACGTTG TACTCTTGGA  
201 TCCAGAAAGT TATTAGATGA AGAAATCAAT CTCAAAGTCA TTATAAGAT  
251 TTAGAAGATA TTAAAATATT TGCGCAGACA AATATTGTTG CTA CTCTCCACG  
301 AGACTATAAT GAAGAAGATT TTAAAGTTAT TGCAAGAAAA GAAGTATTTT  
351 CAACTGGACT AATGATCGAA CTTATTGACA AATGCTTAGT TGA ACTTCTT  
401 TCATCAAGCG ATGTTTCAGA TAGACAAAAA CTTCAATGAT TTGGATTTC  
451 ACTTAAGGGA AATCAATTAG CAAAGACCCA TTTATTAACA GCTCTTTCAA  
501 CTCAAAAGCA GTATTTCTTT CAAGACGAAT GGAACCAAGT TAGAGCAATG  
551 ATTGGAAATG AGCTCTTCG ACATCTCTAC ACTAAATATT TAATATTCCA  
601 GCGAACTTCT GAAGGAAGTC TTGTTCAATT TTGCGGGAAT AACGTTTTTG  
651 ATCATTTGAA AGTCAACGAT AAGTTTGACA AAAAGCAAAA AGGTGGAGCA  
701 GCAGACATGA ATGAACCTCG ATGTTGATCA ACCTGCAAAT ACAATGTCAA  
751 GAATGAGAAA GATCACTTTC TCAACAACAT CAACGTGCCG AATTGGAATA  
801 ATATGAAATC AAGAACCAGA ATATTTTATT GCACTCATTT TAATAGAAAT  
851 AACCAATTCT TCAAAAAGCA TGAGTTTGTG AGTAACAAAA ACAATATTTT  
901 AGCGATGGAC AGAGCTCAGA CGATATTCAC GAATATATTC AGATTTAATA  
951 GAATTAGAAA GAAGCTAAAA GATAAGGTTA TCGAAAAAAT TGCCTACATG  
1001 CTTGAGAAAG TCAAAGATTT TAACTTCAAC TACTATTTAA CAAAATCTTG  
1051 TCCTCTTCCA GAAATTGGC GGAACGGAA AAAAAAATC GAAACTTGA  
1101 TAAATAAAAC TAGAGAAGAA AAGTCGAAGT ACTATGAAGA GCTGTTTACG  
1151 TACACAAGT ATAATAAATG CGTCACACAA TTTATTAATG AATTTTCTA  
1201 CAATATACTC CCCAAAGACT TTTTGACTGG AAGAAACCGT AAGAATTTTC  
1251 AAAAGAAAGT TAAGAAATAT GTGGAACATA ACAAGCATGA ACTCATTAC  
1301 AAAAACTTAT TGCTTGAGAA GATCAATACA AGAGAAATAT CATGGATGCA  
1351 GGTGAGACC TCTGCAAAGC ATTTTATTA TTTTGATCAC GAAAACATCT  
1401 ACGTCTTATG GAAATTGCTC CGATGGATAT TCGAGGATCT CGTCGTCTCG  
1451 CTGATTAGAT GATTTTCTA TGTCACCGAG CAACAGAAAA GTTACTCCAA  
1501 AACCTATTAC TACAGAAAGA ATATTTGGGA CGTCATTATG AAAATGTCAA  
1551 TCGCAGACTT AAAGAAGGAA ACGCTTGCTG AGGTCCAAGA AAAAGAGGTT  
1601 GAAGAATGGA AAAAGTCGCT TGGATTTGCA CCTGGAAAAC TCAGACTAAT  
1651 ACCGAAGAAA ACTACTTTC GTCCAATTAT GACTTTCAAT AAGAAGATTG  
1701 TAAATTCAGA CCGGAAGACT ACAAATTAA CTACAAATAC GAAGTTATTG  
1751 AACTCTCACT TAATGCTTAA GACATTGAAG AATAGAATGT TTAAAGATCC  
1801 TTTTGGATTG GCTGTTTTTA ACTATGATGA TGTAATGAAA AAGTATGAGG  
1851 AGTTTGTGTTG CAAATGGAAG CAAGTTGGAC AACCAAACT CTTCTTTGCA  
1901 ACTATGGATA TCGAAAAGTG ATATGATAGT GTAAACAGAG AAAAACTATC  
1951 AACATTCCTA AAAACTACTA AATTACTTTC TTCAGATTTC TGGATTATGA  
2001 CTGCACAAAT TCTAAAGAGA AAGAATAACA TAGTTATCGA TTCGAAAAAC  
2051 TTTAGAAAGA AAGAAATGAA AGATTATTTT AGACAGAAAT TCCAGAAGAT  
2101 TGCATTGAA GGAGGACAAT ATCCAACCTT ATTCAGTGTT CTGAAAATG  
2151 AACAAAATGA CTAAATGCA AAGAAAACAT TAATTGTTGA AGCAAAGCAA  
2201 AGAAATTATT TTAAGAAAGA TAACTTACTT CAACCAGTCA TTAATATTTG  
2251 CCAATATAAT TACATTAAT TTAATGGGAA GTTTTATAAA CAAACAAAAG  
2301 GAATTCCTCA AGGTCTTTGA GTTTCATCAA TTTTGTATC ATTTTATTAT

FIGURE 9 (cont.)

2351 GCAACATTAG AGGAAAGCTC CTTAGGATTC CTTAGAGATG AATCAATGAA  
2401 CCCTGAAAAT CCAAATGTTA ATCTTCTAAT GAGACTTACA GATGACTATC  
2451 TTTTGATTAC AACTCAAGAG AATAATGCAG TATTGTTTAT TGAGAAACTT  
2501 ATAAACGTAA GTCGTGAAAA TGGATTTAAA TTCAATATGA AGAAACTACA  
2551 GACTAGTTTT CCATTAAGTC CAAGCAAATT TGCAAAATAC GGAATGGATA  
2601 GTGTTGAGGA GCAAAATATT GTTCAAGATT ACTGCGATTG GATTGGCATC  
2651 TCAATTGATA TGAAAACCTCT TGCTTTAATG CCAAATATTA ACTTGAGAAT  
2701 AGAAGGAATT CTGTGTACAC TCAATCTAAA CATGCAAACA AAGAAAGCAT  
2751 CAATGTGGCT CAAGAAGAAA CTAAAGTCGT TTTTAATGAA TAACATTACC  
2801 CATTATTTTA GAAAGACGAT TACAACCGAA GACTTTGCGA ATAAAACCTCT  
2851 CAACAAGTTA TTTATATCAG GCGGTTACAA ATACATGCAA TGAGCCAAAG  
2901 AATACAAGGA CCACTTTAAG AAGAACTTAG CTATGAGCAG TATGATCGAC  
2951 TTAGAGGTAT CTAAAATTAT ATACTCTGTA ACCAGAGCAT TCTTTAAATA  
3001 CCTTGTGTGC AATATTAAGG ATACAATTTT TGGAGAGGAG CATTATCCAG  
3051 ACTTTTTCCT TAGCACACTG AAGCACTTTA TTGAAATATT CAGCACAAAA  
3101 AAGTACATTT TCAACAGAGT TTGCATGATC CTCAAGGCAA AAGAAGCAAA  
3151 GCTAAAAAGT GACCAATGTC AATCTCTAAT TCAATATGAT GCATAGTCGA  
3201 CTATTCTAAC TTATTTTGGA AAGTTAATTT TCAATTTTTG TCTTATATAC  
3251 TGGGGTTTTG GGGTTTTGGG GTTTTGGGG

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FIGURE 10

1 MEVDVDNQAD NHGIHSALKT CEEIKEAKTL YSWIQKVIRC RNQSQSHYKD  
 51 LEDIKIFAQT NIVATPRDYN EEDFKVIARK EVFSTGLMIE LIDKCLVELL  
 101 SSSDVSDRQK LQCFGFQLKG NQLAKTHLLT ALSTQKQYFF QDEWNQVRAM  
 151 IGNELFRHLY TKYLIFQRTS EGTLVQFCGN NVFDHLKVND KFDKKQKGGA  
 201 ADMNEPRCCS TCKYNVKNEK DHFLNNINVP NWNNMKSRTTR IFYCTHFNRN  
 251 NQFFKKHEFV SNKNNISAMD RAQTIFTNIF RFNRIKRLK DKVIEKIAM  
 301 LEKVKDFNFN YYLTKSCPLP ENWRERKQKI ENLINKTREE KSKYYEELFS  
 351 YTTDNKCVTQ FINEFFYNIL PKDFLTGRNR KNFQKKVKKY VELNKHELH  
 401 KNLLLEKINT REISWMQVET SAKHFYYFDH ENIYVLWKLL RWIFEDLVVS  
 451 LIRCFFYVTE QQKSYSKTY YRKNWVIM KMSIADLKKE TLAEVQEKEV  
 501 EEWKKS LGFA PGKLRLIPKK TTFRPIMTFN KKIVNSDRKT TKLTTNTKLL  
 551 NSHMLKTLK NRMFKDPFGF AVFNYDDVMK KYEEFVCKWK QVGQPKLFFA  
 601 TMDIEKCYDS VNREKLSTFL KTTKLLSSDF WIMTAQILKR KNNIVDSKN  
 651 FRKKEMKDYF RQKFQKIALE GGQYPTLFSV LENEQNDLNA KKT LIVEAKQ  
 701 RNYFKKDNLL QPVINICQYN YINFNGKFYK QTKGIPQGLC VSSILSSFYY  
 751 ATLEESSLGF LRDESMNPEN PNVNLLMRLT DDYLLITTQE NNAVL FIEKL  
 801 INVSRENGFK FNMKKLQTSF PLSPSKFAKY GMDSVEEQNI VQDYCDWIGI  
 851 SIDMKTALM PNINLRIEGL CTLNLNMQT KKASMWLKKK LKSFLMNNIT  
 901 HYFRKTITTE DFANKTLNKL FISGGYKYM CAKEYKDHFK KNLAMSSMID  
 951 LEVSKIIYSV TRAFFKYLVC NIKDTIFGEE HYPDFFLSTL KHFIIEFSTK  
 1001 KYIFNRVCM I LKAKEAKLKS DQCQSLIQYD A

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FIGURE 11

1 CCCCCAAACC CCAAACCCC AAAACCCCTA TAAAAAAAGA AAAAATTGAG  
 51 GTAGTTTAGA AATAAAATAT TATTCCCGCA CAAATGGAGA TGGATATTGA  
 101 TTTGGATGAT ATAGAAAATT TACTTCCTAA TACATTCAAC AAGTATAGCA  
 151 GCTCTTGTAG TGACAAGAAA GGATGCAAAA CATTGAAATC TGGCTCGAAA  
 201 TCGCCTTCAT TGACTATTCC AAAGTTGCAA AAACAATTAG AGTTCTACTT  
 251 CTCGGATGCA AATCTTTATA ACGATTCTTT CTTGAGAAAA TTAGTTTTAA  
 301 AAAGCGGAGA GCAAAGAGTA GAAATTGAAA CATTACTAAT GTTTAAATAA  
 351 AATCAGGTAA TGAGGATTAT TCTATTTTTT AGATCACTTC TTAAGGAGCA  
 401 TTATGGAGAA AATTACTTAA TACTAAAAGG TAAACAGTTT GGATTATTTT  
 451 CCTAGCCAAC AATGATGAGT ATATTAAATT CATATGAGAA TGAGTCAAAG  
 501 GATCTCGATA CATCAGACTT ACCAAAGACA AACTCGCTAT AAAACGCAAG  
 551 AAAAAGTTTG ATAATCGAAC AGCAGAAGAA CTTATTGCAT TTACTATTCTG  
 601 TATGGGTTTT ATTACAATTG TTTTAGGTAT CGACGGTGAA CTCCCGAGTC  
 651 TTGAGACAAT TGAAAAAGCT GTTTACAACG GAAGGAATCG CAGTTCTGAA  
 701 AGTTCTGATG TGTATGCCAT TATTTTGTGA ATTAATCTCA AATATCTTAT  
 751 CTCAATTTAA TGGATAGCTA TAGAAACAAA CCAAATAAAC CATGCAAGTT  
 801 TAATGGAATA TACGTAAAT CCTTTGGGAC AAATGCACAC TGAATTTATA  
 851 TTGGATTCTT AAAGCATAGA TACACAGAAT GCTTTAGAGA CTGATTTAGC  
 901 TTACAACAGA TTACCTGTTT TGATTACTCT TGCTCATCTC TTATATCTTT  
 951 AAAAGAAGCA GCGGAAATGA AAAGAAGACT AAAGAAAGAG ATTTCAAAAT  
 1001 TTGTTGATTG TTCTGTAACC GGAATTAACA ACAAGAATAT TAGCAACGAA  
 1051 AAAGAAGAAG AGCTATCACA ATCCTGATTG TTAAAGATTT CAAAAATTCC  
 1101 AGGTAAGAGA GATACATTCA TTAAAATTCA TATATTATAG TTTTTCATT  
 1151 CACAGCTGTT ATTTTCTTTT ATCTTAACAA TATTTTTTGA TTAGCTGGAA  
 1201 GTAAAAAGTA TCAAATAAGA GAAGCGCTAG ACTGAGGTAA CTTAGCTTAT  
 1251 TCACATTCAT AGATCGACCT TCATATATCC AATACGATGA TAAGGAAACA  
 1301 GCAGTCATCC GTTTTAAAAA TAGTGCTATG AGGACTAAAT TTTTAGAGTC  
 1351 AAGAAATGGA GCCGAAATCT TAATCAAAAA GAATTGCGTC GATATTGCAA  
 1401 AAGAATCGAA CTCTAAATCT TTCGTTAATA AGTATTACCA ATCTTGATTG  
 1451 ATTGAAGAGA TTGACGAGGC AACTGCACAG AAGATCATT AAGAAATAAA  
 1501 GTAACTTTTA TTAATTAGAG AATAAACTAA ATTACTAATA TAGAGATCAG  
 1551 CGATCTTCAA TTGACGAAAT AAAAGCTGAA CTAAAGTTAG ACAATAAAAA  
 1601 ATACAAACCT TGGTCAAAAT ATTGAGGAAG GAAAAGAAGA CCAGTTAGCA  
 1651 AAAGAAAAAA TAAGGCAATA AATAAAATGA GTACAGAAGT GAAGAAATAA  
 1701 AAGATTTATT TTTTCAATA ATTTATTGAA AAGAGGGGTT TTGGGGTTTT  
 1751 GGGGTTTTGG GG

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CCCCAAACCCCAAAACCCCTTATAAAAAAGAAAAATTGAGTTAGTTTAGA  
1 ----- 60  
GGGGTTTGGGGTTTGGGGTTTGGGGATATTTTTTCTTTTTTAACCTCCATCAAAATCT  
P Q N P K T P K P L \* K K K K L R \* F R -  
P K T P K P Q N P Y K K R K N C G S L E -  
P K P Q N P K T P I K K E K I E V V \* K -  
AATAAAATATTATCCCGCACAAATGGAGATGGATATTGATTGGATGATATAGAAAATT  
61 ----- 120  
TTATTTTATAATAAGGGCGTGTTTACCTCTACCTATAACTAAACCTACTATATCTTTTAA  
N K I L F P H K W R W I L I W M I \* K I -  
I K Y Y S R T N G D G Y C F G C \* Y R K F -  
\* N I I P A Q M E M D I D L D D I E N L -  
TACTTCTTAATACATTCAACAAGTATAGCAGCTCTTGTAGTGACAAGAAAGGATGCAAAA  
121 ----- 180  
ATGAAGGATTATGTAAGTTGTTTATATCGTCGAGAACATCACTGTCTTTCTACGTTTT  
Y F L I H S T S I A A L V V T R K D A K -  
T S \* Y I Q Q V \* Q L L \* \* Q E R M Q N -  
L P N T F N K Y S S S C S D K K G C K T -  
CATTGAAATCTGGCTCGAAATCGCCTTCATTGACTATTCCAAAGTTGCAAAAACAATTAG  
181 ----- 240  
GTAACTTTACACCGAGCTTTAGCGGAAGTAACTGATAAGGTTTCAACGTTTTTGTTAATC  
H C N L A R N R L H C L F Q S C K N N \* -  
I E I W L E I A F I D Y S K V A K T I R -  
L K S G S K S P S L T I P K L Q K Q L E -  
AGTTCTACTTCTCGGATGCAAAATCTTTATAACGATTCTTCTTGAGAAAAATTAGTTTAA  
241 ----- 300  
TCAAGATGAAGAGCCTACGTTTGAAGTATTGCTAAGAAAGAAGTCTTTTAAATCAAAATT  
S S T S R M Q I F I T I L S C E N \* F \* -  
V L L L G C K S L \* R F F L E K I S F K -  
F Y F S D A N L Y N D S F L R K L V L K -  
AAAGCGGAGAGCAAGAGTAGAAATTGAAACATTACTAATGTTTTAAATAAAATCAGGTAA  
301 ----- 360  
TTTCGCCCTCTCGTTTCTCATCTTTAACTTTGTAATGATTACAAATTTATTTTAGTCCATT  
K A E S K E \* K L K H Y \* C L N K I R \* -  
K R R A K S R N C N I T N V \* I K S G N -  
S G E Q R V E I E T L L M F K \* N Q V M -  
TGAGGATTATTCTATTTTTTAGATCACTTCTTAAGGAGCATTATCGAGAAAAATTACTTAA  
361 ----- 420  
ACTCCTAATAAGATAAAAAATCTAGTGAAGAATTCCTCGTAATACCTCTTTTAAATGAATT  
C G L F Y F L D H F L R S I M E K I T \* -  
E D Y S I F \* I T S \* G A L W R K L L N -  
R I I L F F R S L L K E H Y G E N Y L I -  
TACTAAAAGGTAAACAGTTTGGATTATTTCCCTAGCCAACAATGATGAGTATATTTAAATT  
421 ----- 480  
ATGATTTTCCATTGTCAAACTAATAAAGGGATCGGTTGTTACTACTCATATAATTTAA  
Y \* K V N S L D I Y F P S Q Q C C V Y \* I -  
T K R \* T V W I Y S L A N N D E Y I K F -  
L K G K Q F G L F P \* P T M M S I L N S -

FIGURE 12 (cont.)

CATATGAGAATGAGTCAAAGGATCTCGATACATCAGACTTACCAAAGACAAACTCGCTAT  
 481 ----- 540  
 GTATACCTTACTCAGTTTCCTAGAGCTATGTAGTCTGAATGGTTTCTGTTTGAGCGATA  
 a H M R M S Q R I S I H Q T Y Q R Q T R Y -  
 b I C E C V K G S R Y I R L T K D K L A I -  
 c Y E N E S K D L D T S D L P K T N S L -  
 AAAACGCAAGAAAAAGTTTGATAATCGAACAGCAGAAGAACTTATTGCATTACTATTTCG  
 541 ----- 600  
 TTTTGCCTTCTTTTCAAACCTATTAGCTTGTCTGCTTCTTGAATAACGTAAATGATAAGC  
 a K T Q E K V C \* S N S R R T Y C I Y Y S -  
 b K R K K K F D N R T A E E L I A F T I R -  
 c N A R K S L I I E Q Q K N L L H L L F V -  
 TATGGGTTTTATTACAATTGTTTTAGGTATCGACGGTGAACCTCCGAGTCTTGAGACAAT  
 601 ----- 660  
 ATACCCAAAATAATGTTAACAAAATCCATAGCTGCCACTTGAGGGCTCAGAACTCTGTTA  
 a Y G F Y Y N C F R Y R R C T P E S C D N -  
 b M G F I T I V L G I D G E L P S L E T I -  
 c W V L L Q L F \* V S T V N S R V L R Q L -  
 TGAAAAAGCTGTTTACAACGAAGGAATCGCAGTTCTGAAAGTTCTGATGTGTATGCCAT  
 661 ----- 720  
 ACTTTTTCGACAAATGTTGACTTCCTTAGCGTCAAGACTTCAAGACTACACATACGGTA  
 a C K S C L Q L K E S Q F C K F \* C V C H -  
 b E K A V Y N C R N R S S E S S D V Y A I -  
 c K K L F T T E G I A V L K V L M C M P L -  
 TATTTTGTGAATTAATCTCAAATATCTTATCTCAATTTAATGGATAGCTATAGAAACAAA  
 721 ----- 780  
 ATAAAACACTTAATTAGAGTTTATAGAATAGAGTTAAATTACCTATCGATATCTTTGTTT  
 a Y F V N \* S Q I S Y L N L M D S Y R N K -  
 b I L C I N L K Y L I S I \* W I A I E T N -  
 c F C E L I S N I L S Q F N G \* L \* K Q T -  
 CCAAATAAACCATGCAAGTTTAATGGAATATACGTTAAATCCTTTGGGACAAATGCACAC  
 781 ----- 840  
 GGTTTATTTGGTACGTTCAAATTACCTTATATGCAATTTAGGAAACCCTGTTTACGTGTG  
 a P N X P C K F N G I Y V K S F G T N A H -  
 b Q I N H A S L M E Y T L N P L G Q M H T -  
 c K \* T Y Q V \* W N I R \* I L W D K C T L -  
 TGAATTTATATTGGATTCTTAAAGCATAGATACACAGAATGCTTTAGAGACTGATTAGC  
 841 ----- 900  
 ACTTAAATATAACCTAAGAAATTTCTGATCTATGTGCTTACGAAATCTCTGACTAAATCG  
 a C : Y : G F L K H R Y T E C F R D C F S -  
 b E F I L D S \* S I D T Q N A L E T D L A -  
 c N L Y \* : L K A \* I H R M L \* R L I \* L -  
 TTACAACAGATTACCTGTTTTGATTACTCTTGCTCATCTCTTATATCTTTAAAAGAAGCA  
 901 ----- 960  
 AATGTTGCTCTAATCGACAAAACCTAATGAGAACGAGTAGAGAATATAGAAATTTCTTCGT  
 a L Q Q I T C F D Y S C S S L I S L K E A -  
 b Y N R L P V L I T L A H L L Y L \* K K Q -  
 c T T D Y L F C L L L I S Y I F K R S R -  
 GGCGAAATGAAAAGAGACTAAAGAAAGAGATTTCAAAATTTGTTGATTCTTCTGTAACC  
 961 ----- 1020  
 CCGCTTTACTTTTCTCTGATTTCTTCTCTAAAGTTTAAACAACCTAAGAAGACATTGG  
 a G E H K R R L K K E I S K F V D S S V T -  
 b A X C K E D \* R K R F Q N L L I L L \* P -  
 c R N E X K K T K E R D F K I C C F F C N R -  
 CGAATTAACAACAAGAAATATTAGCAACGAAAAAGAAGAGCTATCACAACTCTGATTC  
 1021 ----- 1080  
 CCTTAATTGTTGTTCTTATAATCGTTGCTTTTTCTTCTCTCGATAGTGTAGGACTAAG  
 a C I N H K N : S N E K E E E L S O S C F -  
 b E L T T R I L A T K K K K S Y H N P D S -  
 c N \* Q Q E Y \* Q P K R R R A I T I L I L -

2025-04-04 14:50:00



FIGURE 12 (cont.)

1681 GTACAGAAGTGAAGAAATAAAAGATTTATTTTTTTCAATAATTTATTGAAAAGAGGGGTT 1740  
-----  
CATGTCTTCACTTCTTTATTTTCTAAATAAAAAAGTTATTAATAACTTTTCTCCCAA

a	V	Q	K	C	R	N	K	R	F	I	F	F	N	N	L	L	K	R	G	V	-
b	Y	R	S	E	E	I	K	D	L	F	F	S	I	I	Y	C	K	E	G	F	-
c	T	E	V	K	K	*	K	I	Y	F	F	Q	*	F	I	E	K	R	G	F	-

1741 TTGGGGTTTTGGGGTTTTGGGG 1762  
-----  
AACCCCAAAACCCCAAAACCCC

a	L	G	F	W	G	F	G	-
b	W	G	F	G	V	L	G	-
c	G	V	L	G	F	W	-	

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FIGURE 13

2 EVDVQNOADNHGIHSALKTCEEIKEAKTLYSWIQKVICRNOQSQSHYKDL 51  
 19 ELELEMOENQNDIQVRVK...IDDPKQY...LVNVTAACLLQEGSYQDK 62  
 52 EDIK:FAOTNIVATPRDYNEEDFKVIARKEVF.STGLMIELIDKCLVELL 100  
 63 DERRVITKALL...EVAESDPEFICQLAVYIRNELYIRTTTNYIVAF. 107  
 101 SSSDVSORQKLQCFGFQKGNQLAKTHLLTALSTQKQYFFQDEWNOVRAM 150  
 108 CVVHKNTQPFIEKYFNKAVLLPNDLLEVCEFAQVLYI 144  
 151 IGNELFRRHLYTKYLIFORTSEGLVQFCGNNVFDHLKVNDKFDKKQKGA 200  
 145 FDATEFKNLY...LDRILSODIRKELTFRKCLQRCVRSKF 181  
 201 ADMNE PRCCSTCKYNVKNEDHFLNNINVPWNMMKSRTIRIFYCTHF 247  
 182 SEFNEYQLGKYCTES...QRKKTMFYLSVTNKQKWDQTKKK... 220  
 248 NRMNQFFKKHEFVSNKNNISAMDRAQTIFTNIFRNRIRKKLKDKVIEKI 297  
 221 RKENLLTKLQAIKESDKSKRETG...DIMNVEDAIKALKPAVMKKI 264  
 298 AYMLEKVKDFNFNYLTCKSCPLPENWRERKQKIENLINKTREESKYEE 347  
 265 AKRONAMK...KHMKAPKIPNSTLESKYLTFKD 294  
 348 LFSYTTDNKCVTQFINEFFYNILPKDFTGRNRKNFQKVKKYVELNKHE 397  
 295 LIKFCHISEP...KERVYKILGKKYPKTEEEYKAAFQDSASAPFN.PE 338  
 398 LIHKNLLEKINTREISWNOVETSAKHFFYFDHENIYVLWKLRLWIFEDL 447  
 339 LAGKRMKIEISKWENELSAKGNTAEVWDNLISSNQLPYMAHLRLNLSN.. 386  
 448 VVSLIRCFYFVTEQOKSYSKTYYYRKNIVDWIMKMSIADLKKETLAEVQE 497  
 387...ILKAGVSD... 394  
 498 KEVEEWKKSGLGFAPGKLRLIPKKTFRPIMTFNKKIVNSDRKTKLTNT 547  
 395...TTHS 398  
 548 KLLNSHMLKTLKNRMFKDPFGFAVFNYYDDVMKKYEEFVCKWKQVQPKL 597  
 399 IVINX...ICEPKAVENSKM 415  
 598 FFATMDIEKCYDSVNREKLSTFLKTTKLLSSDFWIMTAQILKRKNIVID 647  
 416 F.PLOFFSAIEAVN.EAVTKGFKAKK...RENNLKGQIEAVKE..VVE 457  
 648 SKNFRKKENKDYFRQKFQKIALEGGQYPTLFSVLENEQNDLNAKKT LIVE 697  
 458 KTDEEKDM...ELEQTEEGEFVKVNEGIGKQYINSIELAIK 496  
 698 AKQRNYFKKDNLLQPVINICQYNYINFNGKFKYQTKGIPQGLCVSSILSS 747  
 497 IAVNKNLDEIKGHTAIFSDVSGSMSTMSGGAKKYGSVRTCLECALVLGL 546  
 748 FYYATLEESSLGLRDESMNPENPNVLLMRLTDDYLLITTQENNAVLFI 797  
 547 MVKQRCESSEFYIFSSPSSQCNCYLEVDL... 576  
 798 EKLINVSRENGFKFNMKX.LQTSFPLSPSKFAKYGMDSVEEQNIVQDYCD 846  
 577...PCDEL RPSMQKLLQEKGLGGG...TDFPYECIDEWTKNKT HVD 617  
 847 WIGISIDMKTALMPNINLRIEGILCTNLNMQTKKASMWLKKKLKSFLM 896  
 618 NIVILSDMMIAEGYS DINVRGSSIVNSI...KKYKDEVN 653  
 897 NNITHYFRKTITTEDFANKTLNKLFISSGYKYMOCAYKD.HFKKNLAM 945  
 654 PNKIF...AVDLEGY...KCLNLGDEFNENNYIKIFGM 687  
 946 SSNIDLEVSKIISVTRAFFKYLVCNIKDTIFGEEHYPDFLSTLKHFI 995  
 688 SDSI...LKFIKAKQGA...NMVE 706  
 996 IFSTKKYIFNRVC 1008  
 707 VI..KNFALQKIG 717

2005-03-02 10:05:55



FIGURE 15

4 DIDLDDIENLLPNTFNKYSSSCSDKKGCKTLKSGSKSPSLTIPK..... 47  
.....|||.....|...:|...|...:|...|...  
617 NVKSAKIESSSLESLEDIDSLCKSTASCKNLQNVNIIASLLYPNNIQKNP 666  
48 LQKQLEFYFSDANLYNDSFLRKLVLKSGEQRVE....IETLLH 86  
||:|...|:|...:|...:|...:|...:|...:  
667 FNKPNLLFFKQFEQLKNLENVSINCILDQHILNSISEFLEKNKKIKAFIL 716

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FIGURE 16

```
1 MEMDIDLDDIENL. .LPNTFNKYSSSCSDKKGCKTLKSGSKSPS.. 42
| | | | | | | | | | | | | | | | | | | | | |
491 |ELAIKIAVNKNLDEIKGHTAIFSDVSGSMSTSMGGAKKYGSVRTCLEC 540
| | | | | | | | | | | | | | | | | | | | | |
43 |LTIPKLQKQ....LEFYFSDANLYNDSFLRKLVLKSGEQRVEIETLL 85
| : : | | : : : | : : : | : : : | : : : | : : : |
541 ALVLGLMHVKQRCCKSSFYIFSSPSSQCNCYL. EVDLPGDELRPMSHQKLL 589
```

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FIGURE 17

	Motif A	Motif B
Consensus	h--h <h>h</h> h--h--h	h---+ <h>h</h> h---h
telomerase p123	QPKLFFATMDIEKCYDSVNREKLSTFLKTTKL-100-RFYKQTKGIP <h>h</h> LCV <h>h</h> SSILSSFFYATLEESSLGF L	SSILSSFFYATLEESSLGF L
Dong (LINE)	KNRNLHCTYIDYKKA FDSIPHSVLIQVLEIYKIN-28-RQIAIKKGIY <h>h</h> DSLS?JWFCLALNPLSHQLHNDR	SSILSSFFYATLEESSLGF L
al S.c. (group II)	FGGSNWFREVDLKKCFDTISHDLIIKELKRYISD-26-HVPVGPVVCV <h>h</h> APT <h>h</h> SPALCNVAVLRLDORRLAGLA	SSILSSFFYATLEESSLGF L
HIV-RT	LKKCKSVTVLDVGDAYFSVPLDEDFRKYTAFTIP-7-GIRYQYNVLP <h>h</h> WK <h>h</h> SPAI FQSSMTKILEPFRKQN	SSILSSFFYATLEESSLGF L
L8543.12 y <sub>2</sub> 14	VLPELYFMKFDVXSCYDSIPRMECMRILKDALKN-68-KCYIREDDGLF <h>h</h> ESSLSA?IVDLVYDDLLLEFYSEPK	SSILSSFFYATLEESSLGF L

	Motif C	Motif D	Motif E
Consensus	h--Y <h>h</h> DD <h>h</h> h	h-h-h-h-h	h-h-h-h-h
telomerase p123	-14-LMRUTDDYLLITTTQENN-0-AVLFIKLI NVSRN <h>h</h> FK <h>h</h> FN <h>h</h> RLQT-23-QDYCDWIGISI	h-h-h-h-h	h-h-h-h-h
Dong (LINE)	-16-HLIYMDI IKLYAKNDKE-0-MKKLIDTTTIFSNDISMQFGLRCKT-25-KC-YKYLG FQQ	h-h-h-h-h	h-h-h-h-h
al S.c. (group II)	-55-YVRYADDI LIGVLGSKN-2-KIKRDLNNFLNS.IGLTINEERTLI-4-ETPARFLGYNI	h-h-h-h-h	h-h-h-h-h
HIV-RT	-4-IYQYMDDLVVGSHLEIG-1-HRTKIEELRQHLLRWGLTTPDRKHQK-0-EPFLWNGYEL	h-h-h-h-h	h-h-h-h-h
L8543.12 y <sub>2</sub> 14	-8-ILKLA <h>h</h> DDFLIISTDQQQ.....VINIKKLAMC <h>h</h> QKYN <h>h</h> ANR-41-IRSKSSKGIFR	h-h-h-h-h	h-h-h-h-h

FIGURE 18

telomerase p43	LQKQIEEYFSDANLYNDSFLRKLVLKSGEQRVEIETLLM
human La	ICHQIEEYFEGDENLPRDKFLKEQI.KLDEGWVPLEIMIK
Xenopus LaA	ICEQIEEYFEGDENLPRDKFLKQOI.LLDDGWVPLETMIK
Drosophila La	ILRQIEEYFEGDANLNRDKFLREQIGKNEDGWVPLSVLVT
S. c. Lhplp	CLKQIEEYFSEFNFPYDRFLRTTAEK.NDGWVPISTIAT

2003-03-04 10:53:50

FIGURE 19

1 aactcattta attactaatt taatcaacaa gattgataaa aagcagtaaa taaaacccaa  
61 tagatttaatt ttagaaagta tcaattgaaa aatggaaatt gaaaacaact aagcacaata  
121 gccaaaagcc gaaaaattgt ggtgggaact tgaattagag atgcaagaaa accaaaatga  
181 tatataagtt agggtaaga ttgacgatcc taagcaatat ctctggaacg tcactgcagc  
241 atgtttgttg taggaaggta gttactacta agataaagat gaaagaagat atatcatcac  
301 taaagcactt ctgaggtgg ctgagtctga tctgagttc atctgctagt tggcagtcta  
361 catccgtaat gaactttaca tcagaactac cactaactac attgtagcat tttgtgtgt  
421 ccacaagaat actcaacat tcatcgaaaa gtacttcaac aaagcagtac tttgcctaa  
481 tgacttactg gaagtctgtg aattgcata ggttctctat attttgatg caactgaatt  
541 caaaaatttg tatcttgata ggatacttct ataagataat cgtaaggaaac tcaacttccg  
601 taagtgtta caaagatgcg tcagaagcaa gttttctgaa ttcaacgaat actaacttgg  
661 taagtattgc actgaatcct aacgtaagaa aacaatgttc cgttacctct cagttaccaa  
721 caagtaaaag tgggattaaa ctaagaagaa gagaaaagag aatctcttaa ccaaacttta  
781 ggcaataaag gaatctgaag ataagtcaa gagagaaact ggagacataa tgaacgttga  
841 agatgcaatc aaggctttaa aaccagcagt tatgaagaaa atagccaaga gatagaatgc  
901 catgaagaaa cacatgaagg cacctaaaat tcttaactct accttggat caaagtactt  
961 gaccttcaag gatctcatta agttctgcca tatttctgag cctaaagaaa gagtctataa  
1021 gatccttgggt aaaaaatacc ctaagaccga agaggaatac aaagcagcct ttgtgtattc  
1081 tgcatctgca ccttcaatc ctgaattggc tggaaagcgt atgaagattg aaatctctaa  
1141 aacatgggaa aatgaactca gtgcaaaagg caacactgct gaggtttggg ataatttaatt  
1201 ttcaagcaat taactcccat atatggccat gttacgtaac ttgtctaaac tcttaaaagc  
1261 cgggttttca gatactacac actctattgt gatcaacaag atttgtgagc ccaaggccgt  
1321 tgagaactcc aagatgttcc ctcttcaatt ctttagtgcc attgaagctg ttaatgaagc  
1381 agttactaag ggattcaagg ccaagaagag agaaaatatg aatcttaaag gtcaaatcga  
1441 agcagtaaaag gaagtgtgtg aaaaaaccga tgaagagaag aaagatatgg agttggagta  
1501 aaccgaagaa ggagaatttg ttaagtcaa cgaaggaatt ggcaagcaat acattaactc  
1561 cattgaactt gcaatcaaga tagcagttta caagaattta gatgaaatca aaggacacac  
1621 tgcaatcttc tctgatgttt ctggttctat gagtacctca atgtcagggtg gagccaagaa  
1681 gtatggttcc gttcgtactt gtctcgagtg tgcattagtc cttggtttga tggtaaaata  
1741 acgttgtgaa aagtcctcat tctacatctt cagttcacct agttctcaat gcaataagt  
1801 ttactttagaa gttgatctcc ctggagacga actccgtcct tctatgtaaa aacttttgca  
1861 agagaaagga aaacttggtg gtggtactga ttcccctat gagtgcattg atgaatggac  
1921 aaagaataaa actcacgtag acaatatcgt tattttgtct gatatgatga ttgcagaagg  
1981 atattcagat atcaatgtta gaggcagttc cattgttaac agcatcaaaa agtacaagga  
2041 tgaagtaaat cctaactta aaatctttgc agttgactta gaaggttacg gaaagtgcct  
2101 taatctaggt gatgagttca atgaaaacaa ctacatcaag atattcggtg tgagcgattc  
2161 aatcttaaag ttcatctcag ccaagcaagg aggagcaaat atggtcgaag ttatcaaaaa  
2221 ctttgcctt caaaaaatag gacaaaagtg agtttctga gattcttcta taacaaaaat  
2281 ctacccccac tttttgtt tattgcatag ccattatgaa atttaaat taatctatt  
2341 atttaagta ctacatagt ttatgtatcg cagtctatta gcctattcaa atgattctgc  
2401 aaagaacaaa aaagattaaa a

## FIGURE 20

MEIENNQAQQPKAEKLWWELELEMQENQNDIQVRVKIDDPKQYL  
VNVTAACLLQEGSYQDKDERRYIITKALLEVAESDPEFICQLAVYIRNELYIRTTTN  
YIVAFCVVHKNTQPFIEKYFNKAVLLPNDLLEVCEFAQVLYIFDATEFKNLYLDRILS  
QDIRKELTFRKCLQRCVRSKFSEFNEYQLGKYCTESQRKKTMFRYLSVTNKQKWDQTK  
KKRKENLLTKLQAIKESDKSKRETGDIMNVEDAIKALKPAVMKKIAKRQNAMKKHMK  
APKIPNSTLESKYLTFKDLIKFCHISEPKERVYKILGKKYPKTEEEYKAAFGDSASAP  
FNPELAGKRMKIEISKTWENELSAKGNTAEVWDNLISNQLPYMAMLRNLSNILKAGV  
SDTTHSIVINKICEPKAVENSKMFPLQFFSAIEAVNEAVTKGFKAKKRENMNKGGQIE  
AVKEVVEKTDEEKKDMELEQTEEGEFVKVNEGIGKQYINSIELAIKIAVNKNLDEIKG  
HTAIFSDVSGSMSTMSGGAKKYGSVRTCLECALVLGLMVKQRCEKSSFYIFSSPSSQ  
CNKCYLEVDPGDELRPMSMQKLLQEKGKLGGGTDFPYECIDEWTKNKTHVDNIVILSD  
MMIAEGYSDINVRGSSIVNSIKKYKDEVNPNIKIFAVDLEGY GKCLNLGDEFNENNYI  
KIFGMSDSILKFISAKQGGANMVEVIKNFALQKJGQK

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203410 "B54E500T



# FIGURE 21

1 tcaatactat taattaataa ataaaaaaaa gcaactaca aagaaatgt caaggcgtaa  
 61 ctaaaaaaag ccataggctc ctataggcaa tgaacaaat ctgatttig tattacaaa  
 121 tctagaagt tacaaaagcc agattgagca ttataagacc tagtagtaat agatcaaaga  
 181 ggaggatctc aagcttttaa agttcaaaaa ttaagattag gatggaaact ctggcaacga  
 241 tgatgatgat gaagaaaaca actcaataa ataataagaa ttattaagga gagtcaatta  
 301 gattaagtag caagttaat tgataaaaa agttggttct aaggtagaga aagatttgaa  
 361 ttgaacgaa gatgaaaaca aaaagaatgg actttctgaa tagcaagtga aagaagagta  
 421 attaagaacg attactgaag aataggttaa gtattaaaat ttagtattta acatggacta  
 481 ccagttagat ttaaalgaga gtggtggcca tagaagacac agaagagaaa cagattatga  
 541 tactgaaaa tggttgaaa tatctcatga ccaaaaaat tatgtatcaa ttacgccaa  
 601 ctaaaagaca tcatattgtt ggtggcttaa agattatttt aataaaaaa attatgatca  
 661 tcttaatga agcattaaca gactagaaac tgaagccgaa ttctatgcct ttgatgattt  
 721 ttcaaaaaa atcaactta ctaataattc ttactagact gtaaacatag acgttaattt  
 781 tgataataat ctctgtatc tcgcattgct tagattttta ttactactag aaagattcaa  
 841 tattttgaat ataagatctt ctatacaag aaattaatat aatttgaga aaattggtga  
 901 gctacttgaa actatcttcg cagttgtctt ttctcatcgc cacttacaag gcattcattt  
 961 acaagttctt tgcgaagcgt tctaatttt agttaactcc tcatcataaa ttacggttaa  
 1021 agatagctaa ttataggtat actctttctc tacagactta aaattagttg acactaaca  
 1081 agtccaagat tattttaagt tcttataaga attccctcgt ttgactcatg taagctagta  
 1141 ggctatccca gttagtgccta ctaacgctgt agagaacctc aatgttttac ttaaaaaggt  
 1201 caagcatgct aatcttaatt tagtttctat ccctacctaa ttcaatttg atttctactt  
 1261 tgtaattta taacattga aattagagtt tggattagaa ccaaatattt tgacaaaaca  
 1321 aaagcttgaa aatctacttt tgagtataaa ataatacaaaa aatcttaaat tttaagatt  
 1381 aaacttttac acctacgttg ctaagaagac ctccagaaaa cagatattaa aacaagctac  
 1441 aacaatcaaa aatctcaaaa acaataaaaa tcaagaagaa actcctgaaa ctaaagatga  
 1501 aactccaagc gaaagcacia gtggtatgaa atttttgat catctttctg aattaaccga  
 1561 gcttgaagat ttacgcttta acttgtaagc tacccaagaa atttatgata gcttgacaa  
 1621 acttttgatt agatcaacaa atttaagaa gttcaatta agttacaaat atgaaatgga  
 1681 aaagagtaaa atggatacat tcatagatct taagaatatt tatgaaacct taaacaatct  
 1741 taaaagatgc tctgttaata tatcaaatcc tcatggaac atttctatg aactgacaaa  
 1801 taaagattct acttttata aatttaagct gaccttaaac taagaattat aacacgctaa  
 1861 gtatactttt aagtagaacg aattttaatt taataacgtt aaaagtgcaa aaattgaatc  
 1921 ttccāaita gaaagcttag aagatattga tagtcttgc aaatctattg ctcttgtaa  
 1981 aaatttaca aatgttaata ttatgccag ttgtctat cccaacaata tttagaaaa  
 2041 tctttcaat aagcccaatc ttctatttt caagcaattt gaataattga aaaatttga  
 2101 aaatgtatct atcaactgta ttcttgatca gcatatactt aattctattt cagaattctt  
 2161 agaaaagaat aaaaaataa aagcattcat ttgaaaaga tattatttat tacaatatta  
 2221 tcttgattat actaaattat taaaacact tcaatagtta cctgaattaa attagttta  
 2281 cattaattag caattagaag aattgactgt gagtgaagta cataagtaag tatgggaaaa  
 2341 ccacaagcaa aaagctttct atgaaccatt atgtgagttt atcaaagaat catcctaaac  
 2401 cctttagcta atagattttg accaaaacac tgaagtgtat gactctatta aaaagatttt  
 2461 agaactata tctgagtcta agtatcatca ttatttgaga ttgaacccta gttaatctag  
 2521 cagtttaatt aaatctgaaa acgaagaaat ttaagaactt ctcaaagctt gcgacgaaaa  
 2581 aggtgtttta gtaaaagcat actataaatt ccctctatgt ttaccaactg gtacttatta  
 2641 cgattacaat tcagatagat ggtgattaat taaatattag tttaataaa tattaatat  
 2701 tgaatatttc ttgcttatt atttgaataa tacatacaat agtcattttt agtgttttga  
 2761 atatatttta gttatttaatt tcattatttt aagtaataaa ttattttca atcattttt  
 2821 aaaaaatcg

FIGURE 22

MSRRNQKKPQAPIGNETNLDFVLQNLEVYKSQIEHYKTQQQIK  
EEDLKLLKFKNQDQDGNNGNDDDEENNSNKQQELLRRVNQIKQQVQLIKKVGSKVEK  
DLNLNEDENKKNGLSEQQVKEEQLRTITEEQVKYQNLVFNMDYQLDLNESGGHRRHR  
ETDYDTEKWFEISHDQKNYVSIYANQKTSYCWWLKDYFNKNNDHNLNVSINRLETEAE  
FYAFDDFSQTIKLTNNSYQTVNIDVNFNNLCILALLRFLLSLERFNILNIRSSYTRN  
QYNFEKIGELLETIFAVVFSHRHLQGIHLQVPCEAFQYLVNSSSQISVKDSQLQVYSF  
STDKLVDTNKVQDYFKFLQEFPRLTHVSQQAIPVSATNAVENLNVLLKKVKHANLNL  
VSIPTQFNDFYFVNLQHLKLEFGLEPNILTKQKLENLLLSIKQSKNLKFLRLNFYTY  
VAQETSRKQILKQATTIKNLKNNKNQEETPETKDETPSESTSGMKFFDHLSELTELED  
FSVNLQATQEIYDSLHKLLIRSTNLKKFKLSYKYEMEKSKMDTFIDLKNIYETLNNLK  
RCSVNISNPHGNISYELTNKDSTFYKFKLTLNQELQHAKYTFKQNEFQFNNVKSAKIE  
SSSLESLEDIDSLCKSIASCKNLQNVNIIASLLYPNNIQKNPFNKPNNLFFKQFEQLK  
NLENVSINCILDQHILNSISEFLEKNKKIKAFILKRYLLQYYLDYTKLFKTLQQLPE  
LNQVYINQQLEELTVSEVHKQVWENHKQKAFYEPLCEFIKESSQTLQLIDFDQNTVSD  
DSIKKILESISESKYHHYLRLNPSQSSSLIKSENEEIQELLKACDEKGVLVKAYYKFP  
LCLPTGTYYDYNSDRW

FIGURE 23

MKILFEFIQDKLDIDLQTNSTYKENLKC GFHNGLDEILTTCFAL  
PNSRKIALPCLPGDL SHKAVIDHCIIYLLTGELYN NVLTFGYKIARNEDVNNSL FCHS  
ANVNV TLLKGAAWKMFHSLVGTYAFVDLLINYTVIQFNGQFFTQIVGNRCNEPHLPPK  
WVQRSSSSSATAAQIKQLTEPVTNKQFLHKL NINSSSFFPYSKILPSSSSIKKLTDLR  
EAI FPTNLVKIPQRLKVRJNLTLQKLLKRHKRLNYVSILNSICPPLEGTVLDLSHLR  
QSPKERV LKFII VILQKLLPQEMFGSKKNKGKIIKNLNL LLSLPLNGYLPFDSLLKKL  
RLKDFRWLFISDIWFTKHNFENLNQLAICFISWLF RQLIPKIIQTFFYCTEISSTVTI  
VYFRHDTW NKLITPFIVEYFKTYLVENNVCRNHNSY TLSNFNHSKMRJIPKKSNNEFR  
IIAIPCRGADEEEFTIYKENHKNAIQPTQKILEYLRNKRPTSFTKIYSPTQIADRIKE  
FKQRLLKKFNNVLP ELYFMKFDVKSCYDSIPRMECMRILKDALKNENGFFVRSQYFFN  
TNTGVLKLFNVVNASRVKPYEL YIDNVRTVHLSNQDVIN VVEMEIFKTALWVEDKCY  
IREDGLFQGSSLSAPIVDLVYDDLLEFYSEFKASPSQDTLILKLADDFLIISTDQQQV  
INIKKLAMGGFQKYN AKANRDKILAVSSQSDDDTVIQFCAMHIFVKELEVWKHSSTMN  
NFHIRSKSSKGIFRSLIALFNTRISYKTIDTNL NSTNTVLMQIDHVVKNISECYKSAF  
KDLSINVTQNMQFHSFLQR IIEMTVSGCPITKCDPLIEYEV RFTILNGFLESLSNTS  
KFKDNIILLRKEIQHLQAYIYIYIHIVN

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# FIGURE 24

*Oxytricha*  
*Euplates*

LCVSYILSSFYYANLEENALQFLRKESMDPEKPETNLLMRLT  
LCVSSILSSFYYATLEESSLGFLRDESMNPENPNVNLLMRLT

2005-04-01 10:00:00

FIGURE 25

		Motif 0
human		AKFLHWLMSVYVVELLRSPFFYVTETTFQKNR
tez1		ISEIEWLVLGKRSNAXMCLSDFEKRRQIFAEFIYWLNSFIIPILQSFFYITSSDLNR
EST2		LKDFRWLFISD---IWFTKHNFFENLNQLAICFISWLPRLIPKIIQTFFYCTEISSVT-
p123		TREISWMQVET-SAXHPYYFDHEN-IYVLWKLLRWIFEDLVVSLIRCFFYVTEQQKSYSK
		. * . . . . * * *
		Motif 1
human		LFFYRKSVWSKLQSIGIRQHLKRVQLRDVSEAEVRQHREARPALLTSRLRPFKP--DGL
tez1		TVYFRKDIWKLLCRPPI-TSMKMEAFEXINENNVRMDTQK-TTLPPAVIRLLPKK--NTP
EST2		IVYFRHDTWNKLITPFIVEYFKTYLVENNVCRNHNSYTLS--NPNHSMRIIPKKSNEF
p123		TYYYRKNIWDVINKMSI-ADLKKETLAEVQKEVBEWKKS-LGFAPGKLRLIPKK--TTF
		. * . * . * . * . * . *
		Motif 2
human		RPIVNMDYVVGARTFRREKRAERLTSRVKALF-SVLNYERA
tez1		RLITN-LRKRFLLKMGSNKKMLVSTNQTLRPVASILKHLINEESSGIPFKLEVYMKLLTF
EST2		RIIAIPCRGADEEEFTIYKENHKMAIQPTQKILEYLRNKRPTSFTEKIYSPTQIADRIKEF
p123		RPIMTFNKKIVNSDRKTTKLTNTKLLNSHMLKTLKN-RMFKDPPGPAVFHYDDVMKKY
		* * * . . *
		Motif 3 (A)
tez1		KKDLLKHRMFOR-KXYFVRIDIKSCYDRIKQDLMPRIVKK-KLKDPEPVIRKYATIHATS
EST2		RQRLKKFNNVLPELYFMKFDVKSCYDSIPRMECHRIKLD-ALKNENGFFVRSQYFFNTN
p123		EEFVCKWKQVGPQLFFATMDIEKCYDSVNREKLSTFLKTTKLLSSDFWIMTAQILKRKN
		. * . * . * * . . * . *

FIGURE 26

ATTTATACTCATGAAAATCTTATTCGAGTTCATTCAAGACAAGCTTGACATTGATCTACA  
 GACCAACAGTACTTACAAAGAAAATTTAAAATGTGGTCACTTCAATGGCCTCGATGAAAT  
 TCTAACTACGTGTTTTCGCACTACCAAATTCAGAAAAATAGCATTACCATGCCTTCCTGG  
 TGACTIONAAGCCACAAAGCAGTCATTGATCACTGCATCATTTACCTGTTGACGGGCGAATT  
 ATACAACAACGTACTAACATTTGGCTATAAAAATAGCTAGAAATGAAGATGTCAACAATAG  
 TCTTTTTTTGCCATTCTGCAAATGTTAACGTTACGTTACTGAAAGGCGCTGCTTGGAAAAT  
 GTTCCACAGTTTGGTTCGGTACATACGCATTCGTTGATTTATTGATCAATTATACAGTAAT  
 TCAATTTAATGGGCAGTTTTTCACTCAAATCGTGGGTAAACAGATGTAACGAACCTCATCT  
 GCCGCCCAAATGGGTCCAACGATCATCCTCATCATCCGCAACTGCTGCGCAAATCAAACA  
 ACTTACAGAACCAGTGACAAATAACAATTTCTTACACAAGCTCAATATAAATTCCTCTTC  
 TTTTTTTCTTATAGCAAGATCCTTCCTTCATCATCATCTATCAAAAAGCTAACTGACTT  
 GAGAGAAGCTATTTTTTCCACAAATTTGGTTAAAATTCCTCAGAGACTAAAGGTACGAAT  
 TAATTTGACGCTGCAAAAGCTATTAAAGAGACATAAGCGTTTGAATTACGTTTCTATTTT  
 GAATAGTATTTGCCCACCATTGGAAGGGACCGTATTGGACTTGTGCGATTTGAGTAGGCA  
 ATCACCAAAGGAACGAGTCTTGAAATTTATCATTTGTTATTTTACAGAAGTTATTACCCCA  
 AGAAATGTTTGGCTCAAAGAAAAATAAAGGAAAAATTATCAAGAATCTAAATCTTTTATT  
 AAGTTTACCCTTAAATGGCTATTTACCATTGTGATAGTTTGTGAAAAAGTTAAGATTAAA  
 GGATTTTTCGGTGGTTGTTTCAATTTCTGATATTTGGTTTACCAAGCACAATTTTGAAAACCTT  
 GAATCAATTGGCGATTTGTTTCAATTTCTGGCTATTTAGACAACCTAATTCCTAAAATTAT  
 ACAGACTTTTTTTTACTGCACCGAAATATCTTCTACAGTGACAATTGTTTACTTTAGACA  
 TGATACTTGAATAAACTTATCACCCCTTTTATCGTAGAATATTTTAAGACGTACTTAGT  
 CGAAAACAACGTATGTAGAAACCATAATAGTTACACGTTGTCCAATTTCAATCATAGCAA  
 AATGAGGATTATACCAAAAAAAGTAATAATGAGTTCAGGATTATTGCCATCCCATGCAG  
 AGGGGCAGACGAAGAAGAATTCACAATTTATAAGGAGAATCACAAAAATGCTATCCAGCC  
 CACTCAAAAAATTTTAGAATACCTAAGAAACAAAAGGCCGACTAGTTTTACTAAAATATA  
 TTCTCCAACGCAAATAGCTGACCGTATCAAAGAATTTAAGCAGAGACTTTTAAAGAAAT  
 TAATAATGTCTTACCAGAGCTTTATTTTCATGAAATTTGATGTCAAATCTTGCTATGATTC  
 CATACCAAGGATGGAATGTATGAGGATACTCAAGGATGCGCTAAAAAATGAAAATGGGT  
 TTTTCGTTAGATCTCAATATTTCTTCAATACCAATACAGGTGTATTGAAGTTATTTAATGT  
 TGTTAACGCTAGCAGAGTACCAAAACCTTATGAGCTATACATAGATAATGTGAGGACGGT  
 TCATTTATCAAATCAGGATGTTATAAACGTTGTAGAGATGGAAATATTTAAAACAGCTTT  
 GTGGGTTGAAGATAAGTGCTACATTAGAGAAGATGGTCTTTTTTCAGGGCTCTAGTTTATC  
 TGCTCCGATCGTTGATTTGGTGTATGACGATCTTCTGGAGTTTTATAGCGAGTTTAAAGC  
 CAGTCCTAGCCAGGACACATTAATTTTAAAACCTGGCTGACGATTTCTTTATAATATCAAC  
 AGACCAACAGCAAGTGATCAATATCAAAAAGCTTGCCATGGGCGGATTTCAAAAATATAA  
 TCGGAAAGCCAATAGAGACAAAATTTAGCCGTAAGCTCCCAATCAGATGATGATACGGT  
 TATTCAATTTTGTGCAATGCACATATTTGTTAAAGAATTGGAAGTTTGGAAACATTCAAG  
 CACAATGAATAATTTCCATATCCGTTCGAAATCTAGTAAAGGGATATTTTGAAGTTTAAAT  
 AGCGCTGTTTAACTAGAAATCTCTTATAAAAACAATTGACACAAATTTAAATTCACAAA  
 CACCGTTCTCATGCAAATTGATCATGTTGTAAAGAACATTTCGGAATGTTATAAATCTGC  
 TTTTAAAGGATCTATCAATTAATGTTACGCAAAATATGCAATTTTCAATTCGTTCTTACAACG  
 CATCATTGAAATGACAGTCAGCGGTGTCCAATTACGAAATGTGATCCTTTAATCGAGTA  
 TGAGGTACGATTCACCATATTGAATGGATTTTTTGAAAGCCTATCTTCAAACACATCAAA  
 ATTTAAAGATAATATCATTCTTTTGAGAAAGGAAATTCAACACTTGCAAGC

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FIGURE 27

AKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKS VWSKLQSIGIRQHLKR  
VQLRDVSEAEVRQHREARPA LLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKR  
AERLTSRVKALFSVLNYERA

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FIGURE 28

GCCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTC  
TTTCTTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACC  
GGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAA  
GAGGGTGCAGCTGCGGGACGTGTCGGAAGCAGAGGTCAGGCAGCATCGGGA  
AGCCAGGCCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGACG  
GGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCG  
CAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTG TTCAGC  
GTGCTCAACTACGAGCGGGCGCG

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[illegible][illegible]

FIGURE 30

ggtagcgatttactttctttccttcataagcgaattgcttctcgaacgctcctaatactctggaataattttacaagaactcaataacaataccaagtcgaattccaatatgaagg  
 tgttattagtagcgataattttctattttacggctggtaccagataaggacaaaagaacacttctcccccataagacttttacttttataatttacttttcaatatatttcg  
 gggttgcttacttttaacgtggtactgttttagctgctacttctagccaaccggtgtttctaccccgctggtgatatagcttggagtagctcacagaaacttcaaaactt  
 ctgatgagactatattagattcattacagtcggtgcatatttcaacatggagccttacacttttagatgagtcacgctgcatgagtaggtattggatcatccaacggttgcttg  
 aaaaggttgataattattgcaaaatcatgctttagtggtggaatccgcgaagtttttgatgcttcacacgcttagcatgattgagatattcaaaaattctatccactacaa  
 ctctttaaaccggttttattttctattttctatctcatgttgttccaaatagtatcatctctgtattaggcctttttcgttttactctggaatcgactttttcactattccccctaatg  
 aataatctaaattagtttcgcttataattgatagtagtagaaagattggtagtactctggtatgttattagtttaaagatactttgcaaaacatttattagctatcattatataaaa  
 aaaaactataaattataaataatcaatatttgcggtcactattttttaaagcttatgacagtaggacactttgcatatatatagttatgcttaattggttacttgaacttgCAT  
 GACCGAACACCATACCCCCAAAAGCAGGATTCTTCGCTTTCTAGAGAATCAATATGTATACCTATGTAT  
 CCTTAAATGATTATGTACAACCTTGTGAGAGGGTCGCCGGAAGCTCGTATAGCAATATATGCGAA  
 CGCTTGAGAAGCGATGTACAAACGTCCTTTTCTATTTTTCTTCATTGACTGTAGTCGGCTTCGACAGT  
 AAGCCAGATGAAGGTGTTCAATTTTTCTTCTCCAAAATGCTCACAGTCAGAGgtatatataattttgtttgattttttctatttcg  
 ggatagcgaatatatgggcagCTAATAGCGAATGTTGTAAAAACAGATGTTTCGATGAAAAGTTTTGAGCGTCGAAGGA  
 ATCTACTGATGAAAGGGTTTTCCATGgttaaggtattctaattgtgaaatatttaccgtcaattactgtttcaagagattgtatttaaccgataaagAA  
 TCATGAAGATTTTCGAGCCATGCATGTAAACGGAGTACAAAATGATCTCGTTTCTACTTTTCTAATTA  
 CCTTATATCTATACTTGAGTCAAAAAATTGGCAACTTTTGTAGAAAATgtaaataccggttaagattgtgcgactttgaaca  
 agactgacaagtatagTATCGGCAGTGATGCCATGCATTACTTATTATCCAAAGGAAGTATTTTTGAGGCTCTTC  
 CAAATGACAATTACCTTCAGATTTCTGGCATAACCACTTTTTAAAAATAATGTGTTTGAGGAACTGTGT  
 CAAAAAAAAGAAAGCGAACCATTGAAACATCCATTACTCAAAATAAAAGCGCCCGCAAGAAGTTTC  
 CTGGAATAGCATTTCATTAAGTAGGTTAGCATTTTTTACAGGTCATCCTATAAGAAGTTTAAGCAAGgt  
 aactaatactgttatcttcataactaatttagATCTATATTTTAACTTACACTCTATTTGTGATCGGAACACAGTACACATG  
 TGGCTTCAATGGATTTTTCCAAGGCAATTTGGACTTATAAACGCATTTCAAGTGAAGCAATTGCACAA  
 AGTGATTCCACTGGTATCACAGAGTACAGTTGTGCCCAAACGTCCTAAAGGTATACCCTTTAATTGA  
 ACAACAGCAAAGCGACTCCATCGTATTTCTCTATCAAAAGTTTACAACCATTATTGCCCATATATTGA  
 CACCCACGATGATGAAAAAATCCTTAGTTATTCTTAAAGCCGAACCAGGTGTTTGCGTTTCTTCGATC  
 CATTCTTGTTTCGAGTGTTTCTAAATTAATCTGGGGTAACCAAAGGATATTTGAGATAATATTAAGg  
 tattgtataaaattattaccactaacgattttaccagACCTCGAAACTTTCTTGAAATTATCGAGATACGAGTCTTTTAGTTTAC  
 ATTATTTAATGAGTAACATAAAAGgttaatatgccaaatttttaccattaataacaatcagATTTAGAAATTGAATGGCTAGT  
 CCTTGAAAAAAGGTCAAATGCGAAATGTGCTTAAGTGATTTTGAGAAACGCAAGCAAATATTTGCGG  
 AATTCATCTACTGGCTATACAATTCTGTTTATAATACCTATTTTACAATCTTTTTTTTATATCACTGAATC  
 AAGTGATTTACGAAATCGAAGTGTATTTTAGAAAAGATATTTGGAAACTCTTGCGCCGACCCTTTAT  
 TACATCAATGAAAATGGAAGCGTTTGAAAAATAAACGAGgtattttaaggtatttttgcaaaaagcgaatattttcagAACAA  
 TGTTAGGATGGATACTCAGAAAACCTTTGCCTCCAGCAGTTATTCGTCTATTACCTAAGAAGAATAC  
 CTTTCGTCTCATTACGAATTTAAGAAAAAGATTCTTAATAAAAGgtattttaaggtatttttgcaaaaagcgaatattttcagAACAA  
 cagATGGGTTCAAACAAAAAATGTTAGTCAGTACGAACCAAACTTTACGACCTGTGGCATCGATACTG  
 AAACATTTAATCAATGAAGAAAGTAGTGGTATTCCATTTAACTTGAGGTTTACATGAAGCTTCTTACT  
 TTTAAGAAGGATCTTCTTAAGCACCGAATGTTTGgttaattataatgcgcgattcctcattataattttgagCGTAAGAAG  
 TATTTTGACGGATAGATATAAAATCCTGTTATGATCGAATAAAGCAAGATTTGATGTTTCGGATTGTT  
 AAAAAAGAACTCAAGGATCCCGAATTTGTAATTCGAAAGTATGCAACCATAACATGCAACAAGTGACCG  
 AGCTACAAAAAATTTGTTAGTGAGGCGTTTTCTATTgttaagttatttttcattggaatttttaacaaattcttttagTTGATAT  
 GGTGCCTTTTGAAAAAGTCGTGCAGTTACTTTCTATGAAAACATCAGATACTTTGTTTGTTGATTTTGT  
 GGATTATTGGACCAAAAGTTCTTCTGAAATTTTTAAATGCTCAAGGAACATCTCTCTGGACACATTGT  
 TAAAGgtataccaattgtgaattgtaataacactaatgaaactagATAGGAAATTCTCAATACCTTCAAAAAGTTGGTATCCCTC  
 AGGGCTCAATTCTGTCTCTTTTTTGTGTCATTTCTATATGGAAGATTTGATTGATGAATACCTATCGTT  
 TACGAAAAAGAAAGGATCAGTGTTGTTACGAGTAGTCGACGATTTCCTCTTTATAACAGTTAATAAAA  
 AGGATGCAAAAAAATTTTTGAATTTATCTTTAAGAGgtgagttgtgtcattcctaagttctaaccgttgagGATTTGAGAA  
 ACACAATTTTTCTACGAGCCTGGAGAAAACAGTAATAAACTTTGAAAATAGTAATGGGATAATAAACA  
 ATACTTTTTTAATGAAAGCAAGAAAAGAATGCCATTCTTCGGTTTCTCTGTGAACATGAGGTCTCTTG  
 ATACATTGTTAGCATGTCCTAAAATTGATGAAGCCTTATTTAACTCTACATCTGTAGAGCTGACGAAAC  
 ATATGGGGAAATCTTTTTTTTACAAAATTCTAAAGgtatactgtgaactgaataatagctgacaaataatcagATCGAGCCTTGC  
 ATCCTTTGCACAAGTATTTATTGACATTACCCACAATTCAAAATTTCAATTCTTGCTGCAATATATATAG  
 GCTAGGATACTCTATGTGTATGAGAGCACAAGCATACTTAAAAAGGATGAAGGATATATTTATTCCCC  
 AAAGAATGTTCAACGGgtgagtagtatttttaactagaaaagtcattaataaccttagATCTTTTGAATGTTATTGGAAGAAAA  
 ATTTGGAAAAAGTTGGCCGAAATATTAGGATATACGAGTAGGCGTTTCTGTCTCTGCAGAAGTCAA

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FIGURE 30 (cont.)

ATGgtacgtgtcgggtctcgagacttcagcaatattgacacatcagGCTTTTTTGTCTTGGAATGAGAGATGGTTTGAAACCCTCTT  
TCAAATATCATCCATGCTTCGAACAGCTAATATACCAATTTTCAGTCATTGACTGATCTTATCAAGCCGC  
TAAGACCAGTTTTGCGACAGGTGTTATTTTTACATAGAAGAATAGCTGATTAAAtgtcatttcaatttattatatacatcctt  
tattactgggtcttaacaatattattactaagtatagctgacccccaaagcaagcatactataggatttctagtaaagtaaattaatctcgttattagttttgattgacttgtcttt  
atccttatacttttaagaagattgacagtgggtgtgactactgccacatgccattaaacgggagtggttaaacattaaaagtaatacatgaggctaatctcctttcatttag  
aataaggaaagtgggttttctataatgaataatgccgcactaatgcaaaaagcgaagattatcttctaaacaagggggattaagcataccgaaggaaaagagagtaatat  
acccagtgttgtgaagaaagcaaggataatttgaacaagcttctgcagatgacaggctaaatttggtagccgaatttggtaaaagccccaggttatccatgggtggccg  
gccttgctactgagacgaaaagaactaaggatagtttgaataactaatagctcatttaattgtcttatataaggttttgttttctgacttcaatttgcaggggtgaaaagaata  
gtgttaagccattattggattccgaaatagccaaatttcttgggtcctcaaagcgggaagtctaaagaacttattgaagcttatgaggcttcaaaaactcctcctgatttaaggag  
gaatcttccaccgatgaggaaatggatagcttatcagctgctgaggagaagcctaatttttgcaaaaagaaaatatcattgggagacatctcttgatgaatcagatgcgga  
gagtatctccagcggatccttgatgtcaataacttctatttctgaaatgtatggctcactgtcgtctcacttctcgtagctctacgcagtttaagtacc

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# FIGURE 31

EST2 pep	FFYCTEISST VTIVYFRHDT WN----	KLIT P-----FIVE YFK-TYLVEN	40
Euplotes pep	FFYVTEQOKS YSKTYYYRKN IWDVI-MKMS	IAD----LKK ETLA--EVQE	43
Trans of tetrahymen	-----KHKE GSQIFYRKP IWKLVSCLTI	VKVRIQFSEK NKQMKQNFYQ	44
Consensus	FFY.TE..K. .S..YYRK. IW...-KL..	....-F..K .....V..	50
EST2 pep	NVCRNHNSY- -----	TLSNFNHSM RLLPKKSNNE FRLLAIPCRG	79
Euplotes pep	KEVEEWKSL -----	---GFAPCKE RLIPKKITT-- FRRLMTFNKK	78
Trans of tetrahymen	KIQLEEENLE KVEEKLIPED SFQKYPQCKE	RLIPPKGS-- FRRLMTFLRK	92
Consensus	K...E..... -----	....F..GKE RLIPKK.... FRRLMTF.RK	100
EST2 pep	ADEEEFTIYK ENHKNAIQPT OKILEYLRNK	RPTSFTKIYS PTQIADRIKE	129
Euplotes pep	IVNSDRKTTK LTTNTKLLNS HLMLKTLKN-	-----RMFK -DPFGFAVFN	120
Trans of tetrahymen	DKQKNIK--- LNLNQILMDS QLVFRNLKD-	-----ML-G -QKIGYSVFD	130
Consensus	.....K..K LN.N..L..S QL.L..LKN-	-----...IG..VF..	150
EST2 pep	FKQRLKKFN NVL-----	PELYFMKFD VKSCYD	157
Euplotes pep	YD-DVMKKYE EFVCKWKQVG QPKFFATMD	IEKCYD	155
Trans of tetrahymen	NK-QISEKFA QFIEKWKNKG RPLLYVTL-	-----	158
Consensus	.K-...KKF. .F..KWK..G .E..LYF.T.D	...CYD	186

EST2 pep  
Euplotes pep  
Trans of tetrahymen  
Consensus

FIGURE 32

S-1: FFY VTE TTF QKN RLF FYR KSV WSK  
S-2: RQH LKR VQL RDV SEA EVR QHR EA  
S-3: ART FRR EKR AER LTS RVK ALF SVL NYE

A-1: AKF LHW LMS VYV VEL LRS FFY VTE TTF Q  
A-2: LFF YRK SVW SKL QSI GIR QHL KRV QLR DVS  
A-3: PAL LTS RLR FIP KPD GLR PIV NMD YVV

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FIGURE 33

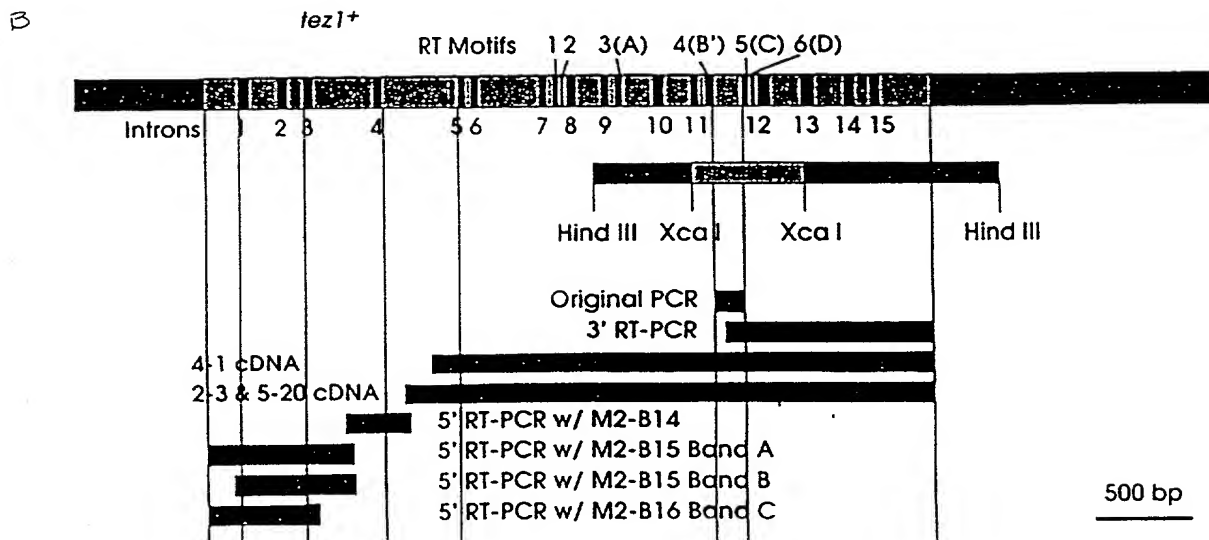
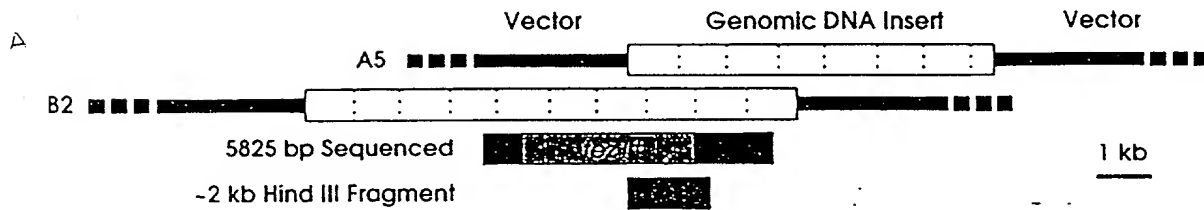


FIGURE 34

Poly 4

	t		t		c			
	t	a	a	g	c	c	t	c g
5'-	cag	acc	aaa	gga	att	cca	taa	gg -3'
	Q	T	K	G	I	P	Q	G

4 (B')

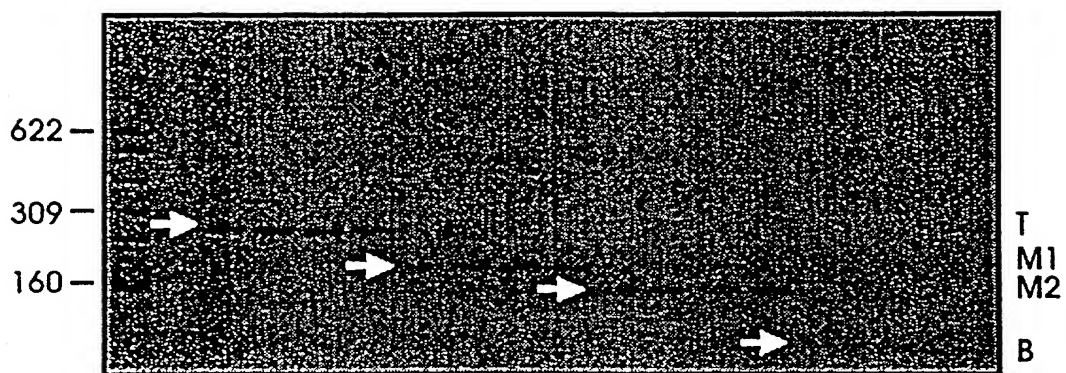
5 (c')

	D	D	Y	L	L	I	T	
3'-	ctg	ctg	atg	gag	gag	tag	tgg	-5'
	a	a	a	a	a	a	a	
				t	t	t	t	
						c	c	

Poly 1

20031101 14:54:00

FIGURE 35



Motif B' (4)  
QTKGIPQG

Motif C (5)  
DDYLLIT

2003-10-10 10:55:00



FIGURE 36

# PCR Product M2 showed Reasonable Match with Other Telomerase Proteins

Ot	LCVSYILSSFYANLEENALQFLRKESMDPEKPETNLLMRLT
Ea_p123	KGIPQGLCVSSILSSFYATLEESSLGFLRDESMNPENPNVNLLMRLTDDYLLIT
Sp_M2	SILSSFLCHFYMEDLIDEYLSFTKKK-----GSVLLRVV
Sc_p103	DGLFQGSSLSAPIVDLVYDDLLEFYSEFKASPS-----QDTLILKLADDFLIIS
	. * . * . * . . . . .

Q K V G I P Q G  
caa aaa gtt ggt atc cct cag gg..... <---Actual Genomic Sequence.

Poly 4  
t t c  
t a a g c c t c g  
cag acc aaa gga att cca taa gg ---->

ag acc aaa gga att cca tca ggC TCA ATT CTG TCA TCT TTT TTG TGT CAT TTC TAT ATG  
tc tgg ttt cct taa ggt agt ccG AGT TAA GAC AGT AGA AAA AAC ACA GTA AAG ATA TAC

K G I P S G S I L S S F L C H F Y M

GAA GAT TTG ATT GAT GAA TAC CTA TCG TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA  
CTT CTA AAC TAA CTA CTT ATG GAT AGC AAA TGC TTT TTC TTT CCT AGT CAC AAC AAT GCT

E D L I D E Y L S F T K K K G S V L L R

GTA GTC gac gac tac ctc ctc atc acc  
CAT CAG ctg ctg atg gag gag tag tgg

V V D D Y L L I T

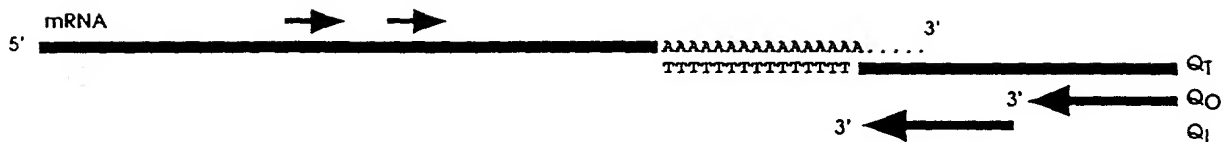
<---- ctg ctg atg gag gag tag tgg  
a a a a a a a a  
t t t t  
c c

Poly 1

.....gac gat ttc ctc ttt ata aca..... <---Actual Genomic Sequence.  
D D F L F I T

FIGURE 37

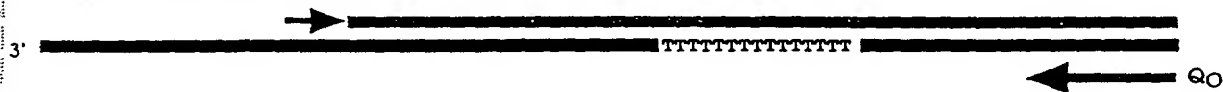
### 3' RT PCR Strategy



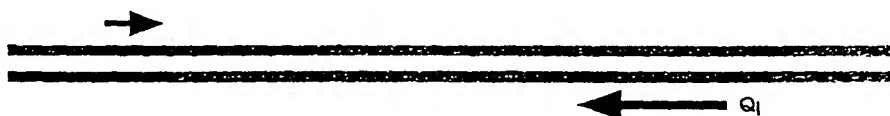
1. Synthesis of cDNA with Q<sub>T</sub> Primer.



2. First Round PCR Using Outside Primer and Q<sub>O</sub> Primer.



3. Second Round PCR Using Inside Primer and Q<sub>I</sub> Primer.



4. Sequence Second Round PCR Products Using Inside Primer or Q<sub>I</sub> Primer.



FIGURE 38

A

-Size Selected Libraries from P. Nurese

- 3 ~ 4 kb
- 5 ~ 6 kb
- 7 ~ 8 kb
- 11 ~ 12 kb

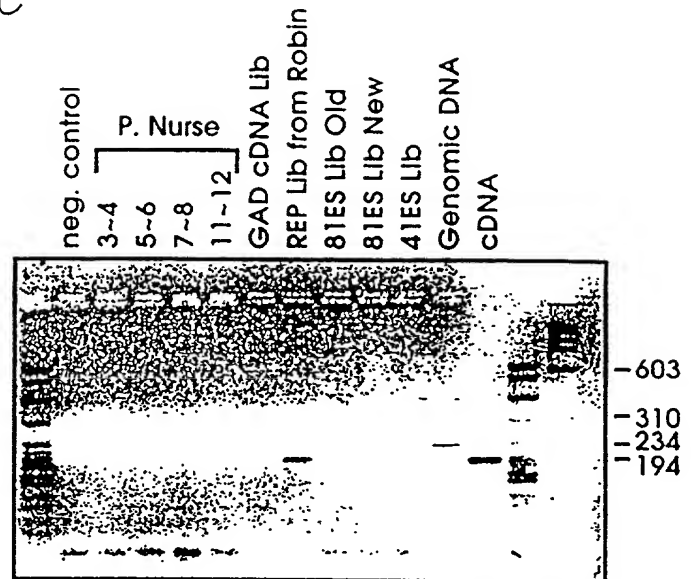
-Libraries from J.A. Wise

- Sau 3a Partial Digest
- Hind III Partial Digest

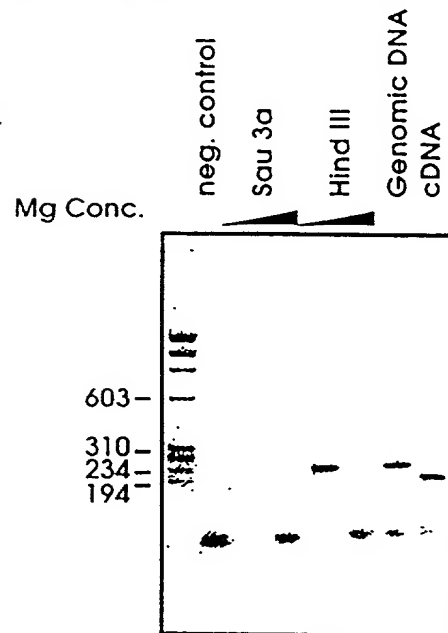
cDNA Libraries

- GAD (Gal Activation Domain) Library
- REP Library from R. Allshire
- REP81ES Library (old)
- REP81ES Library (new)
- REP41ES Library

C



D

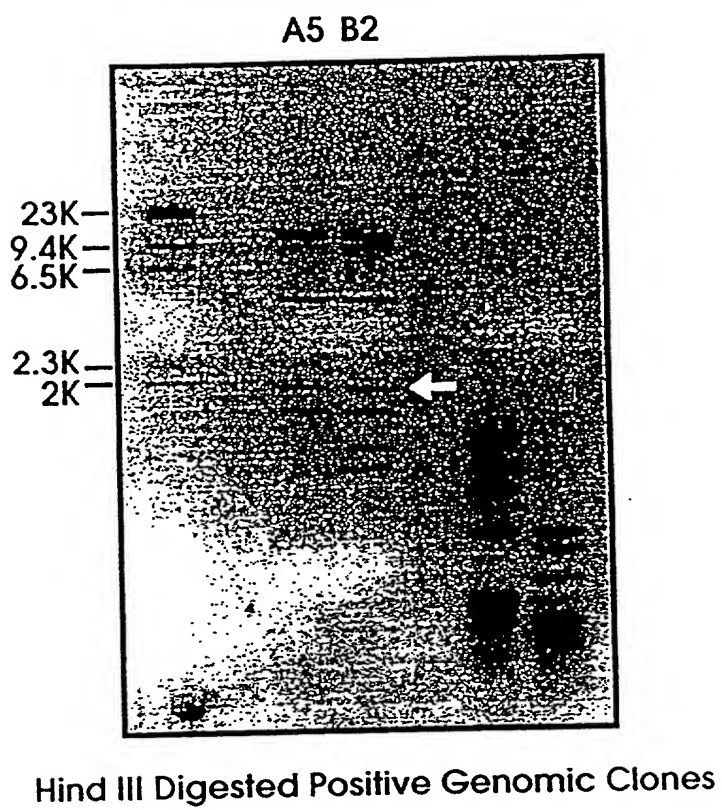


Original PCR  
3' RT-PCR



500 bp

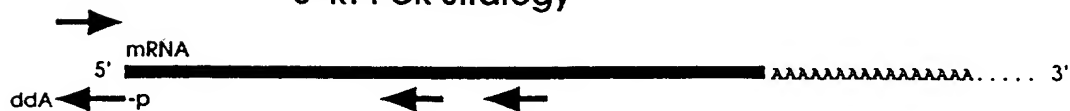
FIGURE 39



20870" 85/EE500T

FIGURE 40

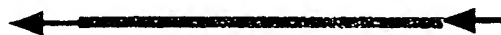
# 5' RT PCR Strategy



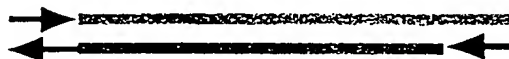
1. Synthesis of cDNA with Specific Downstream Primer.



2. Ligate Oligo with 5'-P and blocked 3' to cDNA using T4 RNA Ligase.



3. First Round PCR



4. Second Round PCR

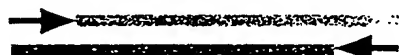


Figure 1. The effect of the concentration of the *Agrobacterium* suspension on the transformation efficiency of *Agrobacterium* strains. The concentration of the *Agrobacterium* suspension was 10<sup>6</sup> cells/ml (A), 10<sup>7</sup> cells/ml (B), 10<sup>8</sup> cells/ml (C), and 10<sup>9</sup> cells/ml (D). The transformation efficiency was determined by the number of transformants per 10<sup>6</sup> cells of the *Agrobacterium* suspension. The data are the mean ± SD of three independent experiments.

### Alignment of RT Domains from Telomerase Catalytic Subunits.

Motif O

S.p. Tezlp (429). WLYNSFIIPILQSFFYITESDDLNRNRTVYFRKDIW ... (35) ...  
S.c. Est2p (366). WLFRQLIPKIIQTFFYCTEISSTVT-IVYFRHDTW ... (35) ...  
E.a. p123 (441). WIFEDLVVSLIRCFYVTEQQKSYSKTYYYRKNIW ... (35) ...

\*                      \*\*\*    \*\*                      \*    \*    \*

Motif 1                      Motif 2                      K  
p hh h K                      hR h                      R

S.p. Tezlp AVIRLLPKK--NTFRLITN-LRKRF ... (61) ...  
S.c. Est2p SKMRIIPKKSNNFRIIAIPCRGAD ... (62) ...  
E.a. p123 GKLRLLPKK--TTFRPIMTFNKKIV ... (61) ...

\*    \*\*\*                      \*\* \*

Motif 3(A) AF  
h hDh GY h

S.p. Tezlp ZKYFVRIDIKSCYDRIKQDLMFRIVK ... (89) ...  
S.c. Est2p ELYFMKFDVKSCYDSIPRMECMRILK ... (75) ...  
E.a. p123 KLFFATMDIEKCYDSVNREKLSTFLK ... (107) ...

\*    \*                      \*\*\*                      \*

Motif 4(B')  
hPQG pP hh h

S.p. Tezlp YLQKVGIPQGSILSSFLCHFYMEDLIDEYLSF ... (6) ...  
S.c. Est2p YIREDGLFQGSSLSAPIVDLVYDDLLEFYSEF ... (8) ...  
E.a. p123 YKQTKGIPQGLCVSSILSSFYATLEESSLGF ... (14) ...

\*                      \*    \*\*                      \*                      \*

Y Motif 5(C)                      Motif 6(D)  
h F DDhhh                      Gh h cK h

S.p. Tezlp VLLRVVDDFLFITVNKKDAKKFLNLSLRGFEKHNFSTSLKTVINFENS . (205)  
S.c. Est2p LILKLADDFLIISTDQQQVINIKKLAMGGFQKYNAAKANKILAVSSQS . (173)  
E.a. p123 LLMLRTDDYLLITTTQENNAVLFIKLINVSRENGFKFNMKKLQTSFPLS . (209)

\*    \*    \*                      \*                      \*                      \*

B

Sp\_Trip1 1 .....MTEHHTPKSRILRFLNENGYVLCY 24  
Sc\_Ea2p2 1 .....MKILFEF 24  
Ea\_p123 1 MEYDVQDQAGDHGHNSALCKEYFKAEATLFSF 24

Sp\_Trip1 26 LNDYVLYLRGSPA.....SNICERLSRSDVOTFS 57  
Sc\_Ea2p2 26 IQDKDLIDLOTN.....TK.....ENLKGKGFHGLD 57  
Ea\_p123 26 IQKYICRGNHSGO.....THK.....OLEDIGFAFNG 57

Sp\_Trip1 34 IFLHSTVYVDFQSKPDQGVYFSPKCSOSEL 67  
Sc\_Ea2p2 34 EILTTCLAPMPSR-KIALPCPLGDSKSHAY 67  
Ea\_p123 42 IVATPRDYNEDEFKVIARKEVYFSTGMLHDK 67

Sp\_Trip1 91 VYKQVDFEDEFERR-HLLMKFSWMHEDFRAM 124  
Sc\_Ea2p2 91 CILLLTQELYN.....NYLTFYKAGHED..... 124  
Ea\_p123 94 CLVLLESSDVSNDROKLGCFYFOLKNGD..... 122

Sp\_Trip1 123 VNGVONOLVSTFPNYHLSILESKHOLLEIL 196  
Sc\_Ea2p2 123 .....VHNSLFCNSAHVNLLESGKMFSLV 196  
Ea\_p123 126 .....LAKTHLLTALSTOKOTFFODEINVRAMI 162

Sp\_Trip1 126 SDAMHYSLSKGSIFEALPNHNYLISIFLFX 164  
Sc\_Ea2p2 126 TYAFVDFLINTYVIOFN-GOFFTIVWRCPFK 164  
Ea\_p123 152 NLFPHHYYTKYLFIOFTSEOTLVFCNHWDFDM 164

Sp\_Trip1 196 HVFEFTVKKKKRKTIEYTSION.....KSARKE 214  
Sc\_Ea2p2 196 HLPPKFWO--RBSSSATAA00.....KOLTER 214  
Ea\_p123 196 LKVNDFKQF-KOKGGAADMHEPCRGSTKYMK 212

Sp\_Trip1 210 WNSISISRFISFYRSSTKFKFDOLYLMNSID 264  
Sc\_Ea2p2 210 .....KQFLKNLINFSSSFFP 264  
Ea\_p123 210 NEK---DNFLNINFPVHNMHMSRTIIFYCTHFM 264

Sp\_Trip1 292 RHYVMHLOWLIFPROFLGIAFOVKOLKHLVPL 344  
Sc\_Ea2p2 292 .....TSKILPSSS.....SIKKLTLEAEIF 372  
Ea\_p123 292 RNT.....NNOFFKKEHYFNKNHNSAMDRAOT 274

Sp\_Trip1 366 YS.....OSTVYPPKRLKYVPLIEOTAKKLHRLS 512  
Sc\_Ea2p2 366 TH.....TIPIDPQV.....VHMLTQKLKHLRLS 512  
Ea\_p123 374 FYNIFRFRHRIKKLKDKYIEKIAYMLEKVKDFM 306

Sp\_Trip1 314 LSKYVNNY.....YID-THODEKLSLTKSPNO..... 342  
Sc\_Ea2p2 314 TVSILSYL.....PLEOTVODKLEIKHLLNKREEK 342  
Ea\_p123 360 FNYVLTSS.....LPENWRERKQKIEHLNKREEK 342

Sp\_Trip1 362 .....FA.....LRSILRVYFLKLI 360  
Sc\_Ea2p2 362 SKYYEELFSYTTONKCTG.....NEFFNYILDK 394  
Ea\_p123 362 .....LQ..... 394

Sp\_Trip1 360 WQHRIKFEIIIDLETFLKRYTESFSLNYMS 392  
Sc\_Ea2p2 360 FGSKNKKEIILNHLNLSPLNGYLPFDSLK 392  
Ea\_p123 392 LTG-RNRHFN.....YKXKXHYHKKHILNHL 392

Sp\_Trip1 392 NIKISIEFLYLOKNSHAKMCLSDYKKKQIFA 426  
Sc\_Ea2p2 392 KRLKQFALFIS.....DIWFFKNHNLNOLA 426  
Ea\_p123 392 KINTREHSMOYETS-AKNFYFDFHNI-VYLV 426

Sp\_Trip1 426 EFILYNSFSLFIPILOS.....SSDLRHRYT 484  
Sc\_Ea2p2 426 CFISLFADROLPIKIOT.....GISSTYV-IV 484  
Ea\_p123 426 KLLRIIFEDLVSLIRCG.....GOKSYSKTY 476

Sp\_Trip1 476 FKDIKLLCRPFTSMKMEAFKIEHNNVRMD 476  
Sc\_Ea2p2 476 FHDINKLITTFVEYFTKTVLSEVYGRNHS 427  
Ea\_p123 476 YKNIIDYIMKSADLKRTLAEYOEKEVEW 476

Sp\_Trip1 492 TOKTTLPPAVILL.....MT.....ILNRKFL 524  
Sc\_Ea2p2 492 .....SHNE.....ILAPCRGAD 524  
Ea\_p123 492 KKSLOFAPOKLLI.....TT.....MTFNKKIL 524

Sp\_Trip1 562 IKMQNSKKMLYSTHQTLPVSAIKKILK 562  
Sc\_Ea2p2 562 EEE---FTYIKHNNKIAOPTQV.....KRR- 562  
Ea\_p123 526 HSD---KRTYKTLTYKLLNSHNNKRN-MF 562

Sp\_Trip1 562 ESSOIFPMLLEVYMKLLTFKKDLLHRMFGR-KK 564  
Sc\_Ea2p2 562 SPFKIYSPSTOADIREFKQKLLKPMHYLPCL 564  
Ea\_p123 562 KQDPFOAFVFNVDYVKKYEFYFC.....GQVQKPL 564

Sp\_Trip1 566 YVYRIKSRIRKODLMFRIVKLLKQPE 616  
Sc\_Ea2p2 566 YMKFYKYSIPMECHNRIIDALKMHNG 616  
Ea\_p123 566 FIAITHIEKSYVNRKLTSTLFTTKLLSSD 616

Sp\_Trip1 616 VIRKATIHATSDRATK..... 624  
Sc\_Ea2p2 616 WYNSQFFPNTNG..... 616  
Ea\_p123 634 FVMTAQILKAKNNIYIDSKNFRKKEKDYFRQK 624

Sp\_Trip1 626 FYSEAFSYDFMVPFEKVLLOS--MKYTSOT 676  
Sc\_Ea2p2 626 .....VLKFLVYNASR--PKPYEY 664  
Ea\_p123 664 FOKIALEGOOQYPTLFSLENGEDLNAAKTIV 664

Sp\_Trip1 692 DFYDVYTKSSSIFKMLKLELSONIYKLGNSG 724  
Sc\_Ea2p2 692 DARTYVYHMOIDVHNMIEFTKALVVEDRC 724  
Ea\_p123 692 EAKORNYFKKNDLLOPVINICOVNYINFNCK 724

Sp\_Trip1 724 LOKYIFKLSIFLCHFMVEDIDEVLSYK 724  
Sc\_Ea2p2 724 IREDLFSLSLAPIVOLVDFYLFESLKRIT 724  
Ea\_p123 724 KOTKTLCLVYSPISFSTYATKESSLGLR 724

Sp\_Trip1 726 KKG.....SVLLR.....FYVHKKDARK 766  
Sc\_Ea2p2 726 SPSSD.....TLILKLA.....FIISTQDOOYV 766  
Ea\_p123 726 DESMPPENFMYHLWRLTYVLTQENHAY 766

Sp\_Trip1 752 FLNLSLQPEKKNHSTSLTYINFNHG..... 766  
Sc\_Ea2p2 752 IKKLLAMGFOKYNAKANDILAVSSD..... 712  
Ea\_p123 766 FIEKLIINSRENGKGFNMKLOTSPLPSKFA 766

Sp\_Trip1 752 .....JHNHTFHESKKRMPFGFSVNMHSLDTLL 676  
Sc\_Ea2p2 752 .....ODTVIOFA--MNIFFLEVYKNSSTN 676  
Ea\_p123 752 KYMGDSVEEONIVODYCWDIGISIDMLALMP 664

Sp\_Trip1 612 ACPKIDEALEFNSTYSIDLKHMGSKFYILRS 676  
Sc\_Ea2p2 746 NMFHRIKSSKGQIFRSIALFTRISYTIOTN 772  
Ea\_p123 746 NINLRIGELICTLFINNMTKCAWMWLKLSF 664

Sp\_Trip1 766 ASFAQVFIIDITHNSKFHNSCCHIVRLGYSNCH 872  
Sc\_Ea2p2 772 DARTYVYHMOIDVHNMIEFTKALVVEDRC 724  
Ea\_p123 766 MNNITNYNFKITTTEDFANKTLNKLISGQY 872

Sp\_Trip1 766 AOAYSKRIIFIPOMFIITOLLNVIORKWK 872  
Sc\_Ea2p2 766 .....YKSAF.....LSSIN-VYDHMGFLOR 872  
Ea\_p123 766 YMOCAKEYHFKKMLASNSMIDLEYSKIVSY 866

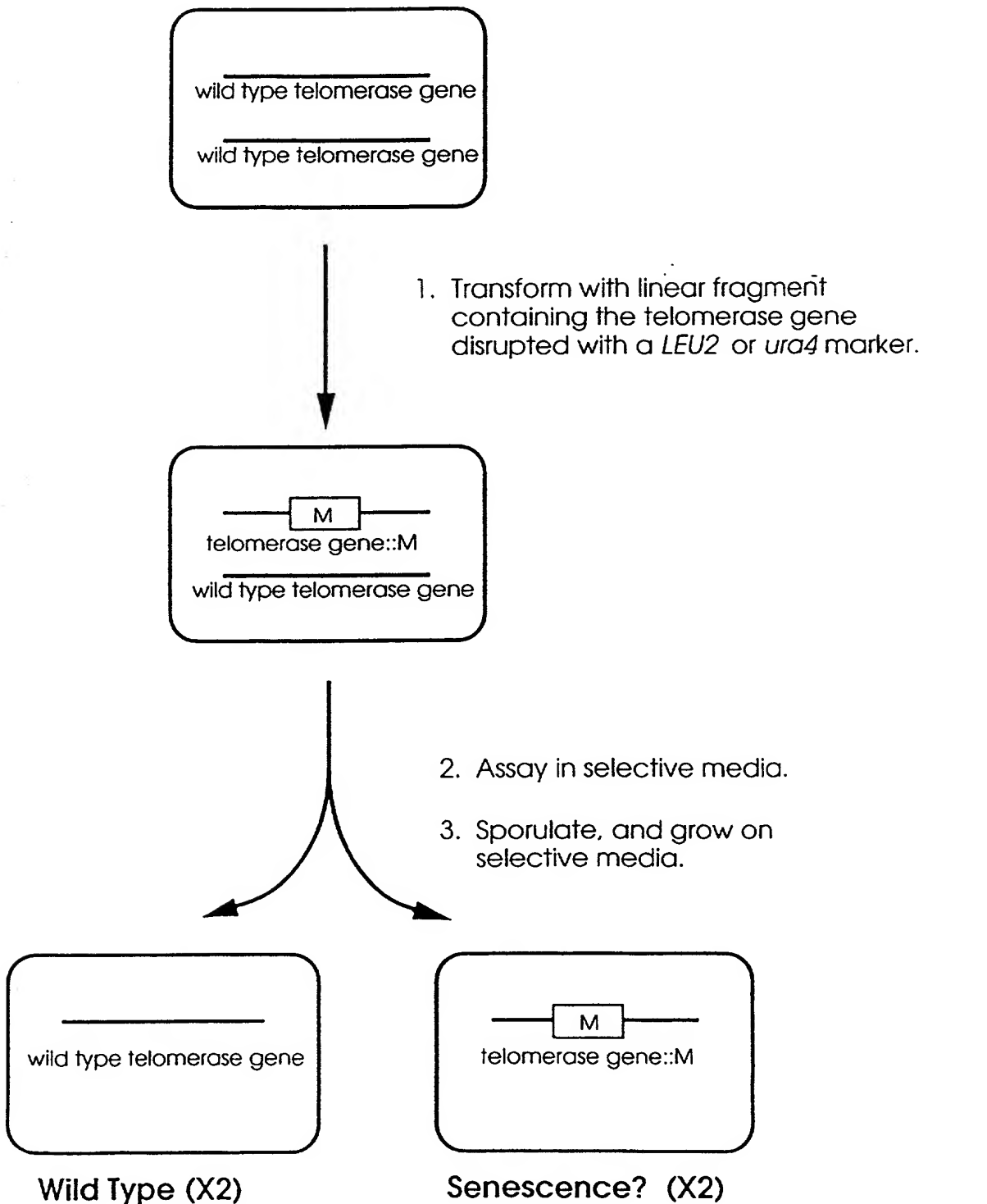
Sp\_Trip1 796 LAELIYDSRFLSSAEVYKFLCLOMRDCKPS 866  
Sc\_Ea2p2 822 TYACQPTIKCOPLEIYEFYHFTLNGFLESK 866  
Ea\_p123 961 TRADFPRYLVKNDIETFIGEENYPOFLSTK 866

Sp\_Trip1 966 FYKHPCEGLIOTVLSLDTLILKPLRYPOLY 872  
Sc\_Ea2p2 966 TS.....KDKNILLKIEIGHQATVIT 872  
Ea\_p123 966 IEIFS---TKKVIHNVYCWILKAEAKKSDOC 862

Sp\_Trip1 966 LNRRIAD- 872  
Sc\_Ea2p2 976 IYIMYIN- 872  
Ea\_p123 966 OSLIQYDA 872

FIGURE 43

# Disruption strategy for the putative telomerase genes.



(These cells will show a senescence phenotype if the disrupted gene encodes a telomerase subunit.)



FIGURE 44

An Example of Confirmation of *tez1* disruption By PCR

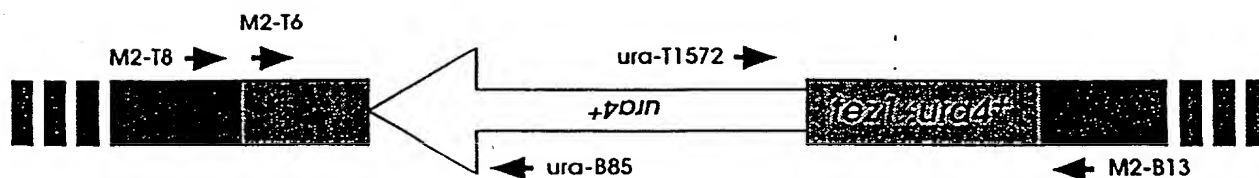
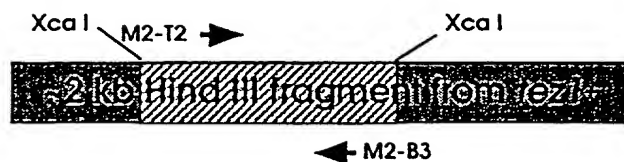
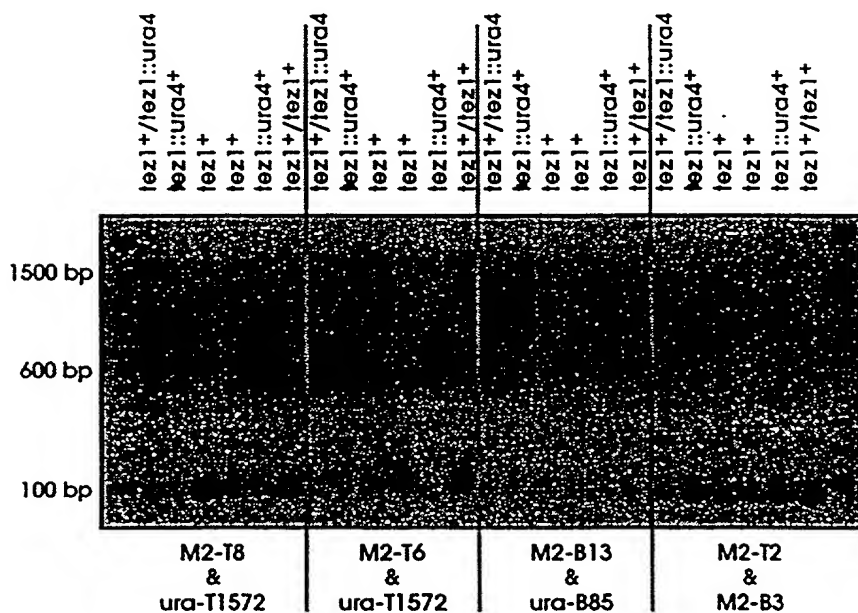


FIGURE 45

*Tez1* disruption causes progressive shortening of telomeres in *S. pombe*

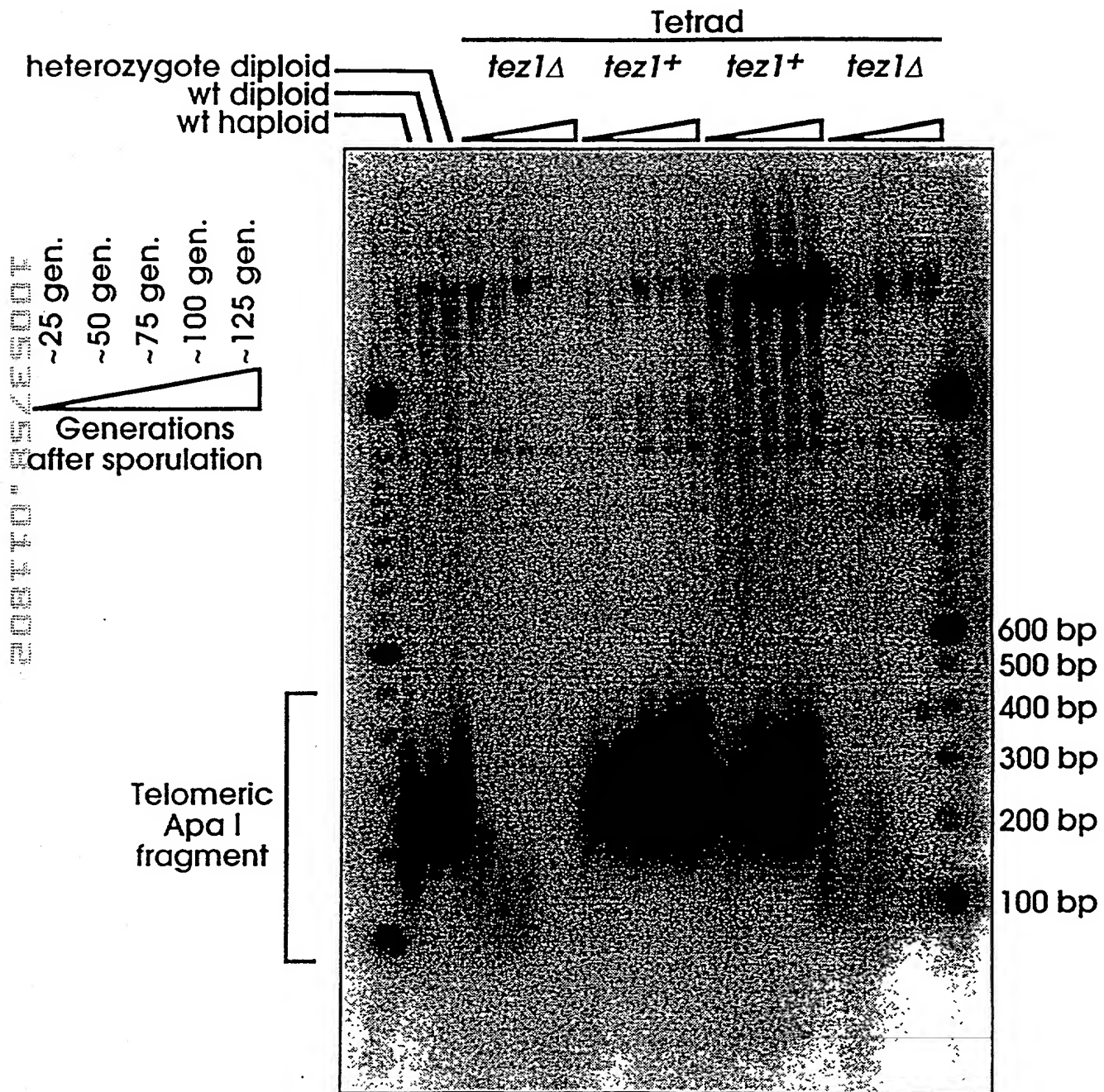


FIGURE 46

1 ggtaccgatttacttttctttcttcataagctaattgcttcctcgaacgctcctaaatctctggaaatattttttacaaga 80  
81 actcaataacaataccaagtcaaattccaatatgaagggtgttatttagtgatcgataatatttctattttatcggtcgta 160  
161 ccaagtataaggacaaaaagaacaacttccttccccctaaagacttttactttattaatttacttttcaaataatatttcg 240  
241 ggttcgcttacttttaacgtggtagctgttttagctgctacttctagccaaccgctgtttctaccccgctcattggatat 320  
321 agctcttggagtagctcacagaaatccttacaaatcttctgatgagactatattagattcattacagtcggtgcatattc 400  
401 ttaacatggagccttacacttttagatgagtcacgctcgcatgatggagtatttgggtatcatccaacggttgccttgaaaag 480  
481 gttgataattatttgcataatcatgtccttagtggtggtaatccgcgaaaagttttttgatgcttgcacacgctctagcatg 560  
561 attgagatattcaaaaatttctatccactacaactcctttaacgcggttttatttttctattttctatttctcatgttggt 640  
641 ccaaatatgtatcatctcgtattaggcttttttccggttttactcctggaatcgtaacctttttcactattccccctaata 720  
721 ataactctaaattagtttgcgttataattgatagtagtagaaaagattggtgattctactcgtgtaattgttattagttttaa 800  
801 gatactttgcataaacatttatttagctatcattatataaaaaaaatcctataattataaatattaatcaatatttgcgggtc 880  
881 actattttattttaaaacggttatgatcagtaggacactttgcatatatatagttatgcttaatggttacttgtaacttgc 958

959 ATG ACC GAA CAC CAT ACC CCC AAA AGC AGG ATT CTT CGC TTT CTA GAG AAT CAA TAT GTA 1018  
1 M T E H H T P K S R I L R F L E N Q Y V 20

1019 TAC CTA TGT ACC TTA AAT GAT TAT GTA CAA CTT GTT TTG AGA GGG TCG CCG GCA AGC TCG 1078  
21 Y L C T L N D Y V Q L V L R G S P A S S 40

1079 TAT AGC AAT ATA TGC GAA CGC TTG AGA AGC GAT GTA CAA ACG TCC TTT TCT ATT TTT CTT 1138  
41 Y S N I C E R L R S D V Q T S F S I F L 60

1139 CAT TCG ACT GTA GTC GGC TTC GAC AGT AAG CCA GAT GAA GGT GTT CAA TTT TCT TCT CCA 1198  
61 H S T V V G F D S K P D E G V Q F S S P 80

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# FIGURE 46 (cont.)

1199 AAA TGC TCA CAG TCA GAG gtatatatatttttgttttgatttttttctattcgggatagctaatatatgggcag 1272  
81 K C S Q S E 86

1273 CTA ATA GCG AAT GTT GTA AAA CAG ATG TTC GAT GAA AGT TTT GAG CGT CGA AGG AAT CTA 1332  
87 L I A N V V K Q M F D E S F E R R R N L 106

1333 CTG ATG AAA GGG TTT TCC ATG gtaagggtatttctaattgtgaaatatttacctgcaattactgtttcaaagaga 1405  
107 L M K G F S M 113

1406 ttgtattttaaccgataaag AAT CAT GAA GAT TTT CGA GCC ATG CAT GTA AAC GGA GTA CAA AAT 1469  
114 N H E D F R A M H V N G V Q N 128

1470 GAT CTC GTT TCT ACT TTT CCT AAT TAC CTT ATA TCT ATA CTT GAG TCA AAA AAT TGG CAA 1529  
129 D L V S T F P N Y L I S I L E S K N W Q 148

1530 CTT TTG TTA GAA AT gtaaataccgggttaagatgttgcgcaactttgaacaagactgacaagtatag T ATC GGC 1601  
149 L L L E I I G 155

1602 AGT GAT GCC ATG CAT TAC TTA TTA TCC AAA GGA AGT ATT TTT GAG GCT CTT CCA AAT GAC 1661  
156 S D A M H Y L L S K G S I F E A L P N D 175

1662 AAT TAC CTT CAG ATT TCT GGC ATA CCA CTT TTT AAA AAT AAT GTG TTT GAG GAA ACT GTG 1721  
176 N Y L Q I S G I P L F K N N V F E E T V 195

1722 TCA AAA AAA AGA AAG CGA ACC ATT GAA ACA TCC ATT ACT CAA AAT AAA AGC GCC CGC AAA 1781  
196 S K K R K R T I E T S I T Q N K S A R K 215

1782 GAA GTT TCC TGG AAT AGC ATT TCA ATT AGT AGG TTT AGC ATT TTT TAC AGG TCA TCC TAT 1841  
216 E V S W N S I S I S R F S I F Y R S S Y 235

1842 AAG AAG TTT AAG CAA G gtaactaatactgttatccttcataactaatttttag AT CTA TAT TTT AAC  
1907  
236 K K F K Q D L Y F N 245

1908 TTA CAC TCT ATT TGT GAT CGG AAC ACA GTA CAC ATG TGG CTT CAA TGG ATT TTT CCA AGG 1967  
246 L H S I C D R N T V H M W L Q W I F P R 265

1968 CAA TTT GGA CTT ATA AAC GCA TTT CAA GTG AAG CAA TTG CAC AAA GTG ATT CCA CTG GTA 2027  
266 Q F G L I N A F Q V K Q L H K V I P L V 285

2028 TCA CAG AGT ACA GTT GTG CCC AAA CGT CTC CTA AAG GTA TAC CCT TTA ATT GAA CAA ACA 2087  
286 S Q S T V V P K R L L K V Y P L I E Q T 305

2088 GCA AAG CGA CTC CAT CGT ATT TCT CTA TCA AAA GTT TAC AAC CAT TAT TGC CCA TAT ATT 2147  
306 A K R L H R I S L S K V Y N H Y C P Y I 325

2148 GAC ACC CAC GAT GAT GAA AAA ATC CTT AGT TAT TCC TTA AAG CCG AAC CAG GTG TTT GCG 2207  
326 D T H D D E K I L S Y S L K P N Q V F A 345

2208 TTT CTT CGA TCC ATT CTT GTT CGA GTG TTT CCT AAA TTA ATC TGG GGT AAC CAA AGG ATA 2267  
346 F L R S I L V R V F P K L I W G N Q R I 365

2268 TTT GAG ATA ATA TTA AAA G gtattgtataaaaattttattaccactaacgattttaccag AC CTC GAA ACT 2336  
366 F E I I L K D L E T 375

FIGURE 46 (cont.)

2337	TTC	TTG	AAA	TTA	TCG	AGA	TAC	GAG	TCT	TTT	AGT	TTA	CAT	TAT	TTA	ATG	AGT	AAC	ATA	AAG	2396	
376	F	L	K	L	S	R	Y	E	S	F	S	L	H	Y	L	M	S	N	I	K	395	
2397	gtaatatgccaaatTTTTTTaccattaattaacaatcag										ATT	TCA	GAA	ATT	GAA	TGG	CTA	GTC	CTT	GGA	2465	
396											I	S	E	I	E	W	L	V	L	G	405	
2466	AAA	AGG	TCA	AAT	GCG	AAA	ATG	TGC	TTA	AGT	GAT	TTT	GAG	AAA	CGC	AAG	CAA	ATA	TTT	GCG	2525	
406	K	R	S	N	A	K	M	C	L	S	D	F	E	K	R	K	Q	I	F	A	425	
2526	GAA	TTC	ATC	TAC	TGG	CTA	TAC	AAT	TCG	TTT	ATA	ATA	CCT	ATT	TTA	CAA	TCT	TTT	TTT	TAT	2585	
426	E	F	I	Y	W	L	Y	N	S	F	I	I	P	I	L	Q	S	F	F	Y	445	
2586	ATC	ACT	GAA	TCA	AGT	GAT	TTA	CGA	AAT	CGA	ACT	GTT	TAT	TTT	AGA	AAA	GAT	ATT	TGG	AAA	2645	
446	I	T	E	S	S	D	L	R	N	R	T	V	Y	F	R	K	D	I	W	K	465	
2646	CTC	TTG	TGC	CGA	CCC	TTT	ATT	ACA	TCA	ATG	AAA	ATG	GAA	GCG	TTT	GAA	AAA-ATA	AAC	GAG	2705		
466	L	L	C	R	P	F	I	T	S	M	K	M	E	A	F	E	K	I	N	E	485	
2706	gtatttttaaagtattttttgcaaaaagctaataatttttcag										AAC	AAT	GTT	AGG	ATG	GAT	ACT	CAG	AAA	ACT	2775	
486											N	N	V	R	M	D	T	Q	K	T	495	
2776	ACT	TTG	CCT	CCA	GCA	GTT	ATT	CGT	CTA	TTA	CCT	AAG	AAG	AAT	ACC	TTT	CGT	CTC	ATT	ACG	2835	
496	T	L	P	P	A	V	I	R	L	L	P	K	K	N	T	F	R	L	I	T	515	
2836	AAT	TTA	AGA	AAA	AGA	TTC	TTA	ATA	AAG	gtattaatttttggtcatcaatgtactttacttctaatactatta										2906		
516	N	L	R	K	R	F	L	I	K											524		
2907	ttagcag		ATG	GGT	TCA	AAC	AAA	AAA	ATG	TTA	GTC	AGT	ACG	AAC	CAA	ACT	TTA	CGA	CCT	GTG	2967	
525			M	G	S	N	K	K	M	L	V	S	T	N	Q	T	L	R	P	V	542	
2968	GCA	TCG	ATA	CTG	AAA	CAT	TTA	ATC	AAT	GAA	GAA	AGT	AGT	GGT	ATT	CCA	TTT	AAC	TTG	GAG	3027	
543	A	S	I	L	K	H	L	I	N	E	E	S	S	G	I	P	F	N	L	E	562	
3028	GTT	TAC	ATG	AAG	CTT	CTT	ACT	TTT	AAG	AAG	GAT	CTT	CTT	AAG	CAC	CGA	ATG	TTT	GG	gtaat	3088	
563	V	Y	M	K	L	L	T	F	K	K	D	L	L	K	H	R	M	F	G		581	
3089	tatataatgcgcgattcctcattattaattttgcag										G	CGT	AAG	AAG	TAT	TTT	GTA	CGG	ATA	GAT	ATA	3155
582												R	K	K	Y	F	V	R	I	D	I	591
3156	AAA	TCC	TGT	TAT	GAT	CGA	ATA	AAG	CAA	GAT	TTG	ATG	TTT	CGG	ATT	GTT	AAA	AAG	AAA	CTC	3215	
592	K	S	C	Y	D	R	I	K	Q	D	L	M	F	R	I	V	K	K	K	L	611	
3216	AAG	GAT	CCC	GAA	TTT	GTA	ATT	CGA	AAG	TAT	GCA	ACC	ATA	CAT	GCA	ACA	AGT	GAC	CGA	GCT	3275	
612	K	D	P	E	F	V	I	R	K	Y	A	T	I	H	A	T	S	D	R	A	631	
3276	ACA	AAA	AAC	TTT	GTT	AGT	GAG	GCG	TTT	TCC	TAT	T	gtaagtttatttttttcattggaattttttaacaa							3343		
632	T	K	N	F	V	S	E	A	F	S	Y	F								643		
3344	attcttttttag		TT	GAT	ATG	GTG	CCT	TTT	GAA	AAA	GTC	GTG	CAG	TTA	CTT	TCT	ATG	AAA	ACA	3405		
644				D	M	V	P	F	E	K	V	V	Q	L	L	S	M	K	T	659		
3406	TCA	GAT	ACT	TTG	TTT	GTT	GAT	TTT	GTG	GAT	TAT	TGG	ACC	AAA	AGT	TCT	TCT	GAA	ATT	TTT	3465	
660	S	D	T	L	F	V	D	F	V	D	Y	W	T	K	S	S	S	E	I	F	679	
3466	AAA	ATG	CTC	AAG	GAA	CAT	CTC	TCT	GGA	CAC	ATT	GTT	AAG	gtataccaattgttgaattgtaataaca						3532		
680	K	M	L	K	E	H	L	S	G	H	I	V	K							692		



3533	cta	gaa	act	ag	ATA	GGA	AAT	TCT	CAA	TAC	CTT	CAA	AAA	GTT	GGT	ATC	CCT	CAG	GGC	TCA	3593
693					I	G	N	S	Q	Y	L	Q	K	V	G	I	P	Q	G	S	708
3594	ATT	CTG	TCA	TCT	TTT	TTG	TGT	CAT	TTC	TAT	ATG	GAA	GAT	TTG	ATT	GAT	GAA	TAC	CTA	TCG	3653
709	I	L	S	S	F	L	C	H	F	Y	M	E	D	L	I	D	E	Y	L	S	728
3654	TTT	ACG	AAA	AAG	AAA	GGA	TCA	GTG	TTG	TTA	CGA	GTA	GTC	GAC	GAT	TTC	CTC	TTT	ATA	ACA	3713
729	F	T	K	K	K	G	S	V	L	L	R	V	V	D	D	F	L	F	I	T	748
3714	GTT	AAT	AAA	AAG	GAT	GCA	AAA	AAA	TTT	TTG	AAT	TTA	TCT	TTA	AGA	G	gtgagttgctgtcattcc				3777
749	V	N	K	K	D	A	K	K	F	L	N	L	S	L	R	G					764
3778	taagttc	taaccg	ttgaag		GA	TTT	GAG	AAA	CAC	AAT	TTT	TCT	ACG	AGC	CTG	GAG	AAA	ACA	GTA		3840
765						F	E	K	H	N	F	S	T	S	L	E	K	T	V		778
3841	ATA	AAC	TTT	GAA	AAT	AGT	AAT	GGG	ATA	ATA	AAC	AAT	ACT	TTT	TTT	AAT	GAA	AGC	AAG	AAA	3900
779	I	N	F	E	N	S	N	G	I	I	N	N	T	F	F	N	E	S	K	K	798
3901	AGA	ATG	CCA	TTC	TTC	GGT	TTC	TCT	GTG	AAC	ATG	AGG	TCT	CTT	GAT	ACA	TTG	TTA	GCA	TGT	3960
799	R	M	P	F	F	G	F	S	V	N	M	R	S	L	D	T	L	L	A	C	818
3961	CCT	AAA	ATT	GAT	GAA	GCC	TTA	TTT	AAC	TCT	ACA	TCT	GTA	GAG	CTG	ACG	AAA	CAT	ATG	GGG	4020
819	P	K	I	D	E	A	L	F	N	S	T	S	V	E	L	T	K	H	M	G	838
4021	AAA	TCT	TTT	TTT	TAC	AAA	ATT	CTA	AG	gtatactgtgtaactgaataatagctgacaaataatcag	A	TCG									4089
839	K	S	F	F	Y	K	I	L	R											S	848
4090	AGC	CTT	GCA	TCC	TTT	GCA	CAA	GTA	TTT	ATT	GAC	ATT	ACC	CAC	AAT	TCA	AAA	TTC	AAT	TCT	4149
849	S	L	A	S	F	A	Q	V	F	I	D	I	T	H	N	S	K	F	N	S	868
4150	TGC	TGC	AAT	ATA	TAT	AGG	CTA	GGA	TAC	TCT	ATG	TGT	ATG	AGA	GCA	CAA	GCA	TAC	TTA	AAA	4209
869	C	C	N	I	Y	R	L	G	Y	S	M	C	M	R	A	Q	A	Y	L	K	888
4210	AGG	ATG	AAG	GAT	ATA	TTT	ATT	CCC	CAA	AGA	ATG	TTC	ATA	ACG	G	gtgagtacttattttaactaga					4274
889	R	M	K	D	I	F	I	P	Q	R	M	F	I	T	D						903
4275	aaagtc	attaatta	accttag		AT	CTT	TTG	AAT	GTT	ATT	GGA	AGA	AAA	ATT	TGG	AAA	AAG	TTG	GCC		4339
904						L	L	N	V	I	G	R	K	I	W	K	K	L	A		917
4340	GAA	ATA	TTA	GGA	TAT	ACG	AGT	AGG	CGT	TTC	TTG	TCC	TCT	GCA	GAA	GTC	AAA	TG	gtacgtgtc		4401
918	E	I	L	G	Y	T	S	R	R	F	L	S	S	A	E	V	K	W			935
4402	ggctctgagacttcagcaatattgacacatcag	G	CTT	TTT	TGT	CTT	GGA	ATG	AGA	GAT	GGT	TTG	AAA								4468
936						L	F	C	L	G	M	R	D	G	L	K					946
4469	CCC	TCT	TTC	AAA																	

FIGURE 46 (cont.)

4666 gctgacccccaaagcaagcatactataggatttctagtaaagtaaaattaatctcggttattagttttgattgacttgtct 4745  
4746 ttatccttatactttttaagaaagattgacagtggttgctgactactgccacatgccattaaacgggagtggttaaaca 4825  
4826 ttaaaagtaatacatgaggctaattctcctttcat ttagaataaggaaagtgggttttctataatgaataatgccgcacta 4905  
4906 atgcaaaaagacgaagattatcttctaacaagggggattaagcatatccgaaggaaaagagagtaatataccagtggt 4985  
4986 gttgaagaaagcaaggataatttgaacaagcttctgcagatgacaggctaaattttggtgaccgaattttggtaaaagc 5065  
5066 cccaggttatccatggtggccggccttgctactgagacgaaaagaaactaaggatagtttgaataactaatagctcattta 5145  
5146 atgtcttatataaggttttgttttttctgacttcaattttgcatgggtgaaaagaaatagtgttaagccattattggat 5225  
5226 tccgaaatagccaaatttcttggttcctcaaagcggaagtctaaagaacttattgaagcttatgaggcttcaaaaactcc 5305  
5306 tcctgatttaaaggaggaatctccaccgatgaggaaatggatagcttatcagctgctgaggagaagcctaattttttgc 5385  
5386 aaaaaagaaaatatcattgggagacatctcttgatgaatcagatgcggagagtatctccagcggatccttgatgtcaata 5465  
5466 acttctattttctgaaatgtatggtcctactgtcgcttcgacttctcgtagctctacgcagttaagtgaccaaggtacc 5544

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FIGURE 47

[illegible]



[illegible]

190	thr	tyr	cys	val	arg	arg	tyr	ala	val	val	200	gln	lys	ala	ala	met
ACG	TAC	TGC	GTG	CGT	CGG	TAT	GCC	GTG	GTC	CAG	CAG	AAG	GCC	GCC	ATG	
					210											
gly	thr	ser	ala	arg	pro	ser	arg	ala	thr	ser	tyr	val	gln	cys		
GGC	ACG	TCC	GCA	AGG	CCT	TCA	AGA	GCC	ACG	TCC	TAC	GTC	CAG	TGC		
220											230					
gln	gly	ile	pro	gln	gly	ser	ile	leu	ser	thr	leu	leu	cys	ser		
CAG	GGG	ATC	CCG	CAG	GGC	TCC	ATC	CTC	TCC	ACG	CTG	CTC	TGC	AGC		
					240											
leu	cys	tyr	gly	asp	met	glu	asn	lys	leu	phe	ala	gly	ile	arg		
CTG	TGC	TAC	GGC	GAC	ATG	GAG	AAC	AAG	CTG	TTT	GCG	GGG	ATT	CGG		
250											260					
arg	asp	gly	leu	leu	leu	arg	leu	val	asp	asp	phe	leu	leu	val		
CGG	GAC	GGG	CTG	CTC	CTG	CGT	TTG	GTG	GAT	GAT	TTC	TTG	TTG	GTG		
					270											
thr	pro	his	leu	thr	his	ala	lys	thr	phe	leu	arg	thr	leu	val		
ACA	CCT	CAC	CTC	ACC	CAC	GCG	AAA	ACC	TTC	CTC	AGG	ACC	CTG	GTC		
280											290					
arg	gly	val	pro	glu	tyr	gly	cys	val	val	asn	leu	arg	lys	thr		
CGA	GGT	GTC	CCT	GAG	TAT	GGC	TGC	GTG	GTG	AAC	TTG	CGG	AAG	ACA		
					300											
val	val	asn	phe	pro	val	glu	asp	glu	ala	leu	gly	gly	thr	ala		
GTG	GTG	AAC	TTC	CCT	GTA	GAA	GAC	GAG	GCC	CTG	GGT	GGC	ACG	GCT		
310											320					
phe	val	gln	met	pro	ala	his	gly	leu	phe	pro	trp	cys	gly	leu		
TTT	GTT	CAG	ATG	CCG	GCC	CAC	GGC	CTA	TTC	CCC	TGG	TGC	GGC	CTG		
					330											
leu	leu	asp	thr	arg	thr	leu	glu	val	gln	ser	asp	tyr	ser	ser		
CTG	CTG	GAT	ACC	CGG	ACC	CTG	GAG	GTG	CAG	AGC	GAC	TAC	TCC	AGC		
340											350					
tyr	ala	arg	thr	ser	ile	arg	ala	ser	leu	thr	phe	asn	arg	gly		
TAT	GCC	CGG	ACC	TCC	ATC	AGA	GCC	AGT	CTC	ACC	TTC	AAC	CGC	GGC		
					360											
phe	lys	ala	gly	arg	asn	met	arg	arg	lys	leu	phe	gly	val	leu		
TTC	AAG	GCT	GGG	AGG	AAC	ATG	CGT	CGC	AAA	CTC	TTT	GGG	GTC	TTG		
370											380					
arg	leu	lys	cys	his	ser	leu	phe	leu	asp	leu	gln	val	asn	ser		
CGG	CTG	AAG	TGT	CAC	AGC	CTG	TTT	CTG	GAT	TTG	CAG	GTG	AAC	AGC		

# FIGURE 47 (cont.)

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                                390
leu gln thr val cys thr asn ile tyr lys ile leu leu leu gln
CTC CAG ACG GTG TGC ACC AAC ATC TAC AAG ATC CTC CTG CTG CAG

400                                410
ala tyr arg phe his ala cys val leu gln leu pro phe his gln
GCG TAC AGG TTT CAC GCA TGT GTG CTG CAG CTC CCA TTT CAT CAG

                                420
gln val trp lys asn pro his phe ser cys ala ser ser leu thr
CAA GTT TGG AAG AAC CCA CAT TTT TCC TGC GCG TCA TCT CTG ACA

430                                440
arg leu pro leu leu leu his pro glu ser gln glu arg arg asp
CGG CTC CCT CTG CTA CTC CAT CCT GAA AGC CAA GAA CGC AGG GAT

                                450
val ala gly gly gln gly arg arg arg pro ser ala leu arg gly
GTC GCT GGG GGC CAA GGG CGC CGC CGG CCC TCT GCC CTC CGA GGC

460                                470
arg ala val ala val pro pro ser ile pro ala gln ala asp ser
CGT GCA GTG GCT GTG CCA CCA AGC ATT CCT GCT CAA GCT GAC TCG

                                480
thr pro cys his leu arg ala thr pro gly val thr gln asp ser
ACA CCG TGT CAC CTA CGT GCC ACT CCT GGG GTC ACT CAG GAC AGC

490                                500
pro asp ala ala glu ser glu ala pro gly asp asp ala asp cys
CCA GAC GCA GCT GAG TCG GAA GCT CCC GGG GAC GAC GCT GAC TGC

                                510
pro gly gly arg ser gln pro gly thr ala leu arg leu gln asp
CCT GGA GGC CGC AGC CAA CCC GGC ACT GCC CTC AGA CTT CAA GAC

520                                530
his pro gly leu met ala thr arg pro gln pro gly arg glu gln
CAT CCT GGA CTG ATG GCC ACC CGC CCA CAG CCA GGC CGA GAG CAG

                                540
thr pro ala ala leu ser arg arg ala tyr thr ser gln gly gly
ACA CCA GCA GCC CTG TCA CGC CGG GCT TAT ACG TCC CAG GGA GGG

550                                560
arg gly gly pro his pro gly leu his arg trp glu ser glu ala
AGG GGC GGC CCA CAC CCA GGC CTG CAC CGC TGG GAG TCT GAG GCC

564
OP
TGA GTGAGTGT TTGGCCGAGGCCTGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGC
CTGAGCGAGTGTCCAGCCAAGGGCTGAGTGTCCAGCACACCTGCGTTTTCACTTCCCCAC

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FIGURE 47 (cont.)

AGGCTGGCGTTCGGTCCACCCCAGGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTCCACT  
CCCCACATAGGAATAGTCCATCCCCAGATTGCGCATTGTTACCCCTTCGCCCTGCCTTCC  
TTTGCCTTCCACCCCCACCATTTCAGGTGGAGACCCTGAGAAGGACCCTGGGAGCTTTGGG  
AATTTGGAGTGACCAAAGGTGTGCCCTGTACACAGGCGAGGACCCTGCACCTGGATGGGG  
GTCCCTGTGGGTCAAATTGGGGGGAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTT  
TTTCAGTTTTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 48

Motif -1  
 Ep p123 ...LVVSLIRCFFYVTEQQKSYSKT...  
 Sp Tez1 ...FIIPILQSFFYITESSDLNRNT...  
 Sc Est2 ...LIPKIIQTFYCTEISSTVTIV...  
 Hs TCP1 ...YVVELLRSSFFYVTETTFQKNRL...  
 consensus FFY TE

Motif 0  
 Ep p123 ...KSLGFAPGKLRRLIPKKT--TFRPIMTFNKKIV...  
 Sp Tez1 ...QKTTLPAPVIRLLPKKN--TFRLLITNLRKRFL...  
 Sc Est2 ...TLSNFNHSMRIIPKKSNEFRIIAIPCRGAD...  
 Hs TCP1 ...ARPALLTSRLRFIPKPD--GLRPIVNMMDYVVG...  
 consensus R PK R I

Motif A  
 Ep p123 ...PKLFFATMDIEKCYDSVNREKLSTFLK...  
 Sp Tez1 ...RKKYFVRIDIKSCYDRIKQDLMFRIVK...  
 Sc Est2 ...PELYFMKFDVKSCYDSIPRMECMRILK...  
 Hs TCP1 ...PELYFVKVDVTGA YDTIPQDRLTEVIA...//...  
 consensus F D YD

Motif B  
 Ep p123 ...NGKFYKQTKGIPQGLCVSSILSSFYYA...  
 Sp Tez1 ...GNSQYLQKVGIPQGSILSSFLCHFYME...  
 Sc Est2 ...EDKCYIREDGLFQGSSLSAPIVDLVYD...  
 Hs TCP1 ...RATSYVQCQGIPQGSILSTLLCSLCYG...  
 consensus G QG S

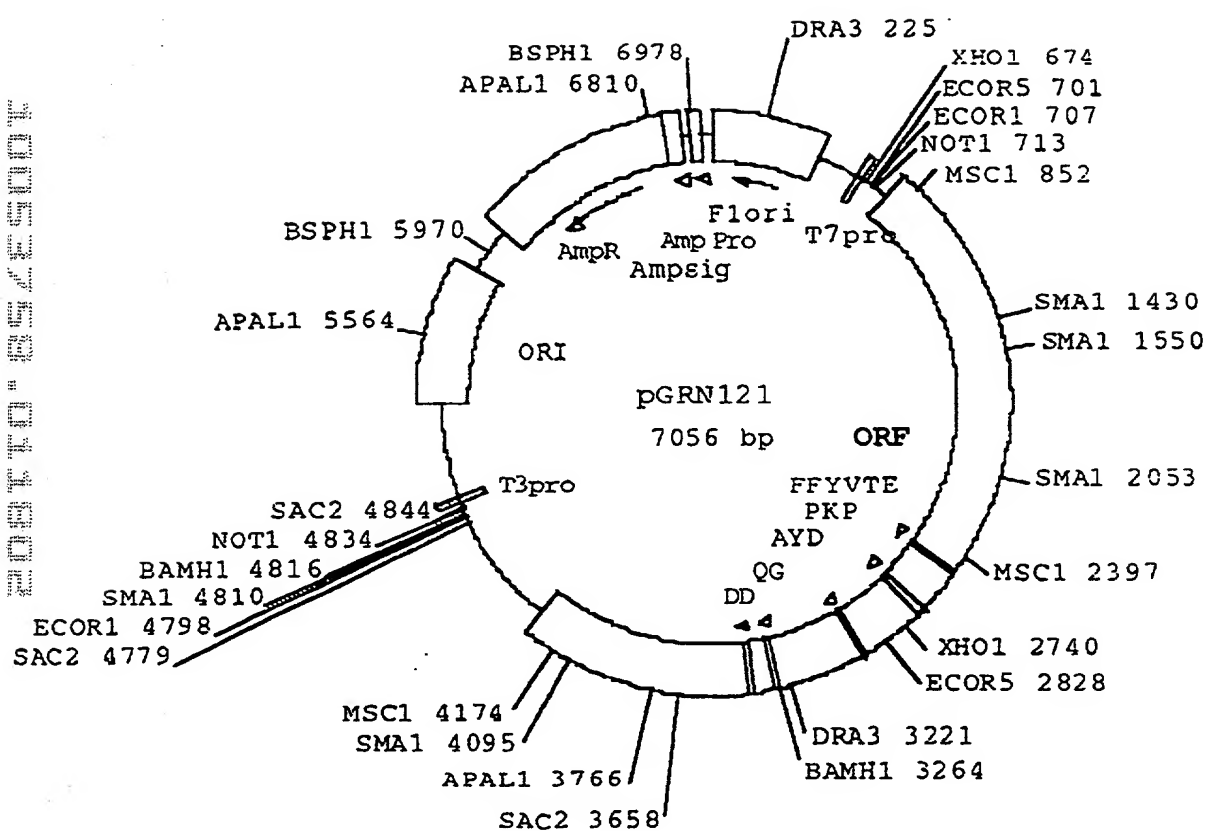
Motif C  
 Ep p123 ...PNVNLLMRLTDDYLLITTQENN...  
 Sp Tez1 ...KKGSVLLRVVDDFLFITVNKKD...  
 Sc Est2 ...SQDTLILKLADDFLIISTDQQQ...  
 Hs TCP1 ...RRDGLLLRLVDDFLLVTPHLTH...  
 consensus DD L

Motif D  
 Ep p123 ...NVSRENGFKFNMKKL...  
 Sp Tez1 ...LNLSLRGFEEKHNFST...  
 Sc Est2 ...KKLAMGGFQKYNAKA...  
 Hs TCP1 ...LRTLVRGVPEYGCVV...  
 consensus G

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FIGURE 49

2003-05-25 10:00



[illegible]

FIGURE 50 (cont.)

2301 GCCCATGGGC ACGTCCGCAA GGCCTTCAAG AGCCACGTCT CTACCTTGAC  
2351 AGACCTCCAG CCGTACATGC GACAGTTCGT GGCTCACCTG CAGGANAACA  
2401 GCCCGCTGAG GGATGCCGTC GTCATCGAGC AGAGCTCCTC CCTGAATGAG  
2451 GCCAGCAGTG GCCTCTTCGA CGTCTTCCTA CGCTTCATGT GCCACCACGC  
2501 CGTGCGCATC AGGGGCAAGT CCTACGTCCA GTGCCAGGGG ATCCCGCAGG  
2551 GCTCCATCCT CTCCACGCTG CTCTGCAGCC TGTGCTACGG CGACATGGAG  
2601 AACAAGCTGT TTGCGGGGAT TCGGCGGGAC GGGCTGCTCC TGC GTTTGGT  
2651 GGATGATTTT TTGTTGGTGA CACCTCACCT CACCCACGCG AAAACCTTCC  
2701 TCAGGACCCT GGTCCGAGGT GTCCCTGAGT ATGGCTGCGT GGTGAACCTG  
2751 CGGAAGACAG TGGTGAACCT CCCTGTAGAA GACGAGGCCC TGGGTGGCAC  
2801 GGCTTTTGT CAGATGCCGG CCCACGGCCT ATTCCCCTGG TCGGCGCTGC  
2851 TGCTGGATAC CCGGACCCTG GAGGTGCAGA GCGACTACTC CAGCTATGCC  
2901 CGGACCTCCA TCAGAGCCAG TCTCACCTT AACC GCGGCT TCAAGGCTGG  
2951 GAGGAACATG CGTCGCAAAC TCTTTGGGGT CTTGCGGCTG AAGTGTCACA  
3001 GCCTGTTTCT GGATTTGCAG GTGAACAGCC TCCAGACGGT GTGCACCAAC  
3051 ATCTACAAGA TCCTCTGCT GCAGGCGTAC AGGTTTCACG CATGTGTGCT  
3101 GCAGTCCCA TTTCATCAGC AAGTTTGGA GAACCCACA TTTTCTCTGC  
3151 GCGTCATCTC TGACACGGCC TCCCTCTGCT ACTCCATCCT GAAAGCCAAG  
3201 AACGCAGGGA TGTCGCTGGG GGCCAAGGGC GCCGCCGGCC CTCTGCCCTC  
3251 CGAGGCCGTG CAGTGGCTGT GCCACCAAGC ATTCCTGCTC AAGCTGACTC  
3301 GACACCGTGT CACCTACGTG CCACTCCTGG GGTCACTCAG GACAGCCCAG  
3351 ACGCAGCTGA GTCGGAAGCT CCCGGGGACG ACGCTGACTG CCCTGGAGGC  
3401 CGCAGCCAAC CCGGCACTGC CCTCAGACTT CAAGACCATC CTGGACTGAT  
3451 GGCCACCCGC CCACAGCCAG GCCGAGAGCA GACACCAGCA GCCCTGTCAC  
3501 GCCGGGCTCT ACGTCCCAGG GAGGGAGGGG CGGCCACAC CCAGGCCCGC  
3551 ACCGCTGGA GTCTGAGGCC TGAGTGAGTG TTTGGCCGAG GCCTGCATGT  
3601 CCGGCTGAAG GCTGAGTGT CCGCTGAGGC CTGAGCGAGT GTCCAGCCAA  
3651 GGGCTGAGTG TCCAGCACAC CTGCCGTCTT CACTTCCCCA CAGGCTGGCG  
3701 CTCGGCTCCA CCCCAGGGCC AGCTTTTCCT CACCAGGAGC CCGGCTTCCA  
3751 CTCCCCACAT AGGAATAGTC CATCCCCAGA TTCGCCATTG TTCACCCCTC  
3801 GCCCTGCCCT CCTTTGCCCT CCACCCAC CATCCAGGTG GAGACCCTGA  
3851 GAAGGACCCT GGGAGCTCTG GGAATTTGGA GTGACCAAAG GTGTGCCCTG  
3901 TACACAGGCG AGGACCCTGC ACCTGGATGG GGGTCCCTGT GGGTCAAATT  
3951 GGGGGGAGGT GCTGTGGGAG TAAATACTG AATATATGAG TTTTTCAGTT  
4001 TTGAAAAAAA AAAAAAAAAA AAAAAAAAAA

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FIGURE 51

GCAGGCGCTGGTTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCCGCCACCCCGCGATGCC  
 1 -----+-----+-----+-----+-----+ 60  
 CTTGCCGACGCGAGGACGACGCGTGCACCCCTTCGGGACCGGGGCGCGTGGGGCGCTACGG  
 a A A I R P A A H V G S P C F G H P R D A -  
 b Q R C V L L R T W E A L A P A T P A M P -  
 c S A A S C C A R G K P W F R P P F R C R -  
 GCGGCTCCCGGCTGCGGAGCGGTGCGCTCCCTGCTGCGCAGCCACTACCGGAGGTGCT  
 61 -----+-----+-----+-----+ 120  
 CGCGGAGGGGCGACGCGCTCGGCACGCGAGGGACGACGCGTGGGTGATGGCGCTCCACGA  
 a A R S P L F S R A L P A A Q P L P R G A -  
 b R A P R C R A V R S L L K S H Y R E V L -  
 c A L P A A E P C A P C C A A T T A R C C -  
 GCGGCTGGCCAGTTGCTGCGGCGCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGGG  
 121 -----+-----+-----+-----+ 180  
 CGCGGACCGGTGCAAGCACGCCGCGGACCCCGGGTCCCGACCGCCGACACGTGGCGCT  
 a A A G H V R A A P G A P G I A A G A A R -  
 b P L A T F V R R L G P Q G W R L V Q R G -  
 c R W P R S C G A W G P R A C G W C S A G -  
 GGACCCGGCGGCTTTCCGCGCGNTGGTGGCCCCANTGCTGCTGGTGGCGCTGGGANGN  
 181 -----+-----+-----+-----+ 240  
 CCTGGGCGCGGAAAGGGCGCGNACCACCGGGTACCGNACACCGCACCGGCGCGCTNUN  
 a G P G G F P R ? G G P ? ? G V R A L G ? -  
 b D P A A F R A ? V A ? C ? V C V P W ? ? -  
 c T R R L S A R W W P ? A W C A C P G ? ? -  
 ANGCGNGCCCCCGCGCGCCCCCTTCCTCCGCGAGGTGCTGCTGAANGANGTGGTGG  
 241 -----+-----+-----+-----+ 300  
 TNCNGCGCGGGGCGCGGGGAGGAAGCGGTCCACAGGACGGACTTNCINGACCGCG  
 a ? A A F R R P L L P P G V L P E ? ? G G -  
 b ? ? P P A A P S F R Q V S C L ? ? L V A -  
 c G ? P P P P P P S A R C P A \* ? ? W W P -  
 CCGAGTCTGCANANGCTGTGCGGANCCTGGCGGCGAANAACGTGCTGGCTTCGGCTTGG  
 301 -----+-----+-----+-----+ 360  
 GGCTCACGAGTNTNCGACACGCTNCGCGCGCGCTTNTTGCACGACCGAAGCGAAGCG  
 a P S A A ? A V R ? R R E ? R A G L R L R -  
 b P V L ? ? L C ? R G A ? N V L A P G P A -  
 c E C C ? ? C A ? A A R ? T C W P S A S R -  
 GCTGCTGGAAGGGGCGCGGGGGCCCCCGCGGCTTTCACCCACGAGTGGCGAGCTA  
 361 -----+-----+-----+-----+ 420  
 CGACGACCTGCGCGGGGCGCGGGGGGGGGGCTCCGAAAGTGGTGGTGGCACCGGTGAT  
 a A A G R G P R G P P R G L H H Q R A Q L -  
 b L L D G A R G G F P E A F T T S V R S Y  
 c C W T G P A G A P F R F S P P A C A A T -

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FIGURE 51 (cont.)

421 CCTGCCCAACACGGTGAACGACGCACTGCGGGGAGCGGAGGCTGCGGGCTGCTGCTGG  
-----+-----+-----+-----+-----+-----+-----+-----+ 480  
GGACGGGTGTGTGCACTGGCTGCGTGACGCGCCCTCTGCCCCGACCCCGAAGACGACGCG

a P A Q H G D R R T A G E F G V G A A A A -  
b L P N T V T D A I R G S G A W G L L L K -  
c C P T R \* F T H C G G A G R G G C C C A -

491 CCGCGTGGGGACGACGCTGCTGGTTCACCTGCTGGCAGCTTCCGCTNINITTCTGCTGCT  
-----+-----+-----+-----+-----+-----+-----+-----+ 540  
GGCCCAACCGCTGCTGCAAGACCAAGTGGAGACCGTGGAGCGCGCNANAAACACGACCA

a P R C R R R A G S P A G T L R ? ? C A G -  
b R V G D D V L V H L L A R C A ? F V L V -  
c A W A T T C W F T C W H A A R ? L C W W -

541 GGNITCCACCTGCGCTACCAAGTGTGCGGGCCGCGCTGTACCAAGCTCGGCGCTGCNAC  
-----+-----+-----+-----+-----+-----+-----+-----+ 600  
CCNAGGCTGACGCGGATGGTNCACACGCCCGGGGGACATGCTGACGCCCCGACGCTC

a G S Q L R L P ? V R A A A V P A R R C ? -  
b ? P S C A Y ? V C G P P L Y Q L G A A T -  
c ? F A A P T ? C A G R R C T S S A L ? L -

601 TCAGGCCCCGGCCCCGCCACACCTANTGACCCCCAAGCCTCTGGGATCCAAAGCGCCT  
-----+-----+-----+-----+-----+-----+-----+-----+ 650  
AGTCCGGGGCGGGGGGGTGTGTGATNACCTGGGCTTNGCAGACCCCTAGATTTCGCGGA

a S C P A P A T R ? W T R ? R L G S N G P -  
b Q A R P P P H A ? G P E ? V W D P T G L -  
c R P G P R H T L ? D F ? A S G I Q R A W -

661 GGAACCATAGCGTCAAGGAGGCCCCGCTCCCCCTCGGCTGCCACCCCCGGGTGCCAGGAC  
-----+-----+-----+-----+-----+-----+-----+-----+ 720  
CCTTGGTATGCAAGTCCCTCGGGCCCCAGGGGACCCGACGGTGGGGGCCAAGCTCTCTC

a G T I A S C R P C S P W A A S P G C E E -  
b E P \* R Q G G R C P P G L P A F G A R R -  
c N H S V R E A G V P L G C Q P R V R G G -

721 GCGCGGUCACAGTGCAGCGGAAGTCTGCCGTGCCCCAAGAAGCCCCAGGGGTGGCGCTGC  
-----+-----+-----+-----+-----+-----+-----+-----+ 780  
CGCGCCCCCGTCAAGTCCGCTTCAGACGGCAACGGGTTCCTCGGGTCCGACCGGGAOS

a A R G Q C Q P K S A V A Q E A Q A W R C  
b R G G S A S R S L P L P K R P R R G A A  
c A G A V F A E V C R C P R G P G V A L ? -

781 CCTTGAGCCCGACCCGACCCCGCTTGGCCAGCGTCTCGGCTCACCCGGGACGGACGCT  
-----+-----+-----+-----+-----+-----+-----+-----+ 840  
GGGACTGCGCTCTGCGGGCAACCCGTCCCCAGGACCCGGGTGGGCCCCCTCTGCGG

a P - A C A D A R W A C V L G F F G Q D A -  
b P E P E R T F V G Q G S W A H P C R T P -  
c L S R S G R P I G R G P G P T R A C R L -

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FIGURE 51 (cont.)

TGGACCGAGTGACCGTGGTTTCTGTGTGGTGTACCTGCCACACCCGCCAAGAAGCCAC  
 841 -----+-----+-----+-----+-----+-----+-----+-----+ 900  
 ACCTGCTCACTGGCACCAGACACACACAGTGGACGGTCTGGGGGGCTTCTTCTGGTG

a W T E \* P W F L C G V T C Q T R R R S H -  
 b G P S D R G P C V V S P A R P A E E A T  
 c D R V T V V S V W C H L P D P P K K P F -

CTCTTGGAGGGTCCGCTCTCTGGCACGGGCTCTCCACCCATCCGTGGGCGGCGACCA  
 901 -----+-----+-----+-----+-----+-----+-----+ 960  
 CAGAAACCTCCACCGGAGAGACCGTGGCGGTGAGGGTGGGTAGGCACCCGGCGGTCTG

a L F G G C A L W H A P L P P I R G P F A  
 b S L E G A L S C T R H S H P S V G R Q H -  
 c L W R V R S L A R A T P T H P W A A S T -

CCACCGGGGGCCCCATCCACATCGCGGCCACACGTCTTGGGACACGCTTGTCTCCCTG  
 961 -----+-----+-----+-----+-----+-----+-----+ 1020  
 GGTGCGCCCGCGGCTAGGTGTAGCGCGGTTGTTGCGAGACCTGTGCGGAACAGCGGCG

a P R C P P I H I A A T T S W D T F C P P  
 b H A G P P S T S R P P R P G T R L V P E  
 c T R A F H P H R G H H V L G H A L S P G -

GTGTAGCGGAGACCAAGCACTTCTCTACTCTCAGCGGACAAGNACACTGGCGNCCCTC  
 1021 -----+-----+-----+-----+-----+-----+-----+ 1080  
 CACATCGGCTCTGTTCTGAAGGAGATGAGGAGTCCGCTGTTCTNTGTGACGCGGGGAG

a V Y A E T K H F L Y S S C D K ? T A ? L -  
 b C T P R P S T S S T P Q A T ? T L R P S -  
 c V R R D Q A L P L L L R E Q ? H C ? P P -

CTTCTACTCAATATATCTGAGGCGCAGCCTGACTGGCGTTGGGAGGTTCTGTGGAGACA  
 1081 -----+-----+-----+-----+-----+-----+-----+ 1140  
 GAAGGATGAGTTATATAGACTCCGGGTGGGACTGACCGCAAGCCCTCCAGGACCTCTCT

a L P T Q Y I \* G P A \* L A F G R F V E T  
 b F L L N I S E A Q P D W R S G G S W R ? -  
 c S Y S I Y L R P S L T G V R E V R G D ? -

NTCTTTCTGTTTCAGGCCTTGGATGCCAGGATTCGCCGAGGTTGCCCCGCTGCCCCA  
 1141 -----+-----+-----+-----+-----+-----+-----+ 1200  
 NAGAPAGACCAAGGTTCGGAACCTTACGGTCTTAAGGGGCTTCAACGGGGCGACGGGT

a P F L V P G L G C Q D S P Q V A P P A P -  
 b S F W F Q A L D A R I P R R L P R L P Q -  
 c L S G S R P W M P G F P A G C P A C P S -

GCGNTACTGCCAATGCGGCGCCTGTTCTGTGAGCTGCTTGGAACCCAGCGCAGTGCCC  
 1201 -----+-----+-----+-----+-----+-----+-----+ 1260  
 CGCNATACCGTTTACGCGGGGACAAGACTTCGACGAACCTTGGGTGGCGGTACCGG

a A ? L A N A A P V S G A A W E P R A V P -  
 b R Y W Q M R F L F L E L L G N H A Q C P -  
 c ? T G K C G P C F W S C L G T T R S A F -

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[illegible][illegible]

12345678910111213141516171819202122232425262728293031323334353637383940414243444546474849505152535455565758596061626364656667686970717273747576777879808182838485868788899091929394959697989910010110210310410510610710810911011111211311411511611711811912012112212312412512612712812913013113213313413513613713813914014114214314414514614714814915015115215315415515615715815916016116216316416516616716816917017117217317417517617717817918018118218318418518618718818919019119219319419519619719819920020120220320420520620720820921021121221321421521621721821922022122222322422522622722822923023123223323423523623723823924024124224324424524624724824925025125225325425525625725825926026126226326426526626726826927027127227327427527627727827928028128228328428528628728828929029129229329429529629729829930030130230330430530630730830931031131231331431531631731831932032132232332432532632732832933033133233333433533633733833934034134234334434534634734834935035135235335435535635735835936036136236336436536636736836937037137237337437537637737837938038138238338438538638738838939039139239339439539639739839940040140240340440540640740840941041141241341441541641741841942042142242342442542642742842943043143243343443543643743843944044144244344444544644744844945045145245345445545645745845946046146246346446546646746846947047147247347447547647747847948048148248348448548648748848949049149249349449549649749849950050150250350450550650750850951051151251351451551651751851952052152252352452552652752852953053153253353453553653753853954054154254354454554654754854955055155255355455555655755855956056156256356456556656756856957057157257357457557657757857958058158258358458558658758858959059159259359459559659759859960060160260360460560660760860961061161261361461561661761861962062162262362462562662762862963063163263363463563663763863964064164264364464564664764864965065165265365465565665765865966066166266366466566666766866967067167267367467567667767867968068168268368468568668768868969069169269369469569669769869970070170270370470570670770870971071171271371471571671771871972072172272372472572672772872973073173273373473573673773873974074174274374474574674774874975075175275375475575675775875976076176276376476576676776876977077177277377477577677777877978078178278378478578678778878979079179279379479579679779879980080180280380480580680780880981081181281381481581681781881982082182282382482582682782882983083183283383483583683783883984084184284384484584684784884985085185285385485585685785885986086186286386486586686786886987087187287387487587687787887988088188288388488588688788888989089189289389489589689789889990090190290390490590690790890991091191291391491591691791891992092192292392492592692792892993093193293393493593693793893994094194294394494594694794894995095195295395495595695795895996096196296396496596696796896997097197297397497597697797897998098198298398498598698798898999099199299399499599699799899910001001100210031004100510061007100810091010101110121013101410151016101710181019102010211022102310241025102610271028102910301031103210331034103510361037103810391040104110421043104410451046104710481049105010511052105310541055105610571058105910601061106210631064106510661067106810691070107110721073107410751076107710781079108010811082108310841085108610871088108910901091109210931094109510961097109810991100110111021103110411051106110711081109111011111112111311141115111611171118111911201121112211231124112511261127112811291130113111321133113411351136113711381139114011411142114311441145114611471148114911501151115211531154115511561157115811591160116111621163116411651166116711681169117011711172117311741175117611771178117911801181118211831184118511861187118811891190119111921193119411951196119711981199120012011202120312041205120612071208120912101211121212131214121512161217121812191220122112221223122412251226122712281229123012311232123312341235123612371238123912401241124212431244124512461247124812491250125112521253125412551256125712581259126012611262126312641265126612671268126912701271127212731274127512761277127812791280128112821283128412851286128712881289129012911292129312941295129612971298129913001

C S T T S G R G A P A S W A P L C W A W -  
A O L E A G A A P R P F G R I C A G P G -  
L N Y E R A R R P G L L G A S V L G I D -

FIGURE 51 (cont.)

ACGATATCCACAGGCGCTGGCGCACTTGTGCTGCGTGTGCGGCGCCAGGACCCGCGCC  
 2101 -----+-----+-----+-----+-----+ 2150  
 TGCTATAGGTGTCCCGGACCGCTGGAAGCAAGACACAGCCCGGGTCTCTGGGGCGG

a T I S T G P G A P S C C V C G P R T R R -  
 b R Y F Q G L A H L R A A C A G P G P A A -  
 c D I H R A W R T F V L R V R A Q D F F P -

CTCAGCTGTACTTTGTCAAGGTGGATGTGAGCGCGCGGTACGACACCATCCCCAGGACA  
 2161 -----+-----+-----+-----+-----+ 2220  
 GACTCGACATGAACAATTCCACCTACACTGCCCGGCGATGCTGTGGTAGGGGTCTCTGT

a I S C T L S R W M \* R A R T T F S F R T -  
 b \* A V L C Q G G C D G R V R H H P P G Q  
 c E L Y F V K V D V T G A Y D T I P Q D R -

GCCTCAGGAGGTGATGCCAGCATCATCAAAACCCAGAACACGTACTGCGTCCGTCCGT  
 2221 -----+-----+-----+-----+-----+ 2280  
 CCGAGTGCCCTCCAGTAGCGGTCTAGTAGTTTGGGGTCTTGTGCATGACGCAAGCAAGCA

a G S R R S S P A S S N P R T R T A C V G -  
 b A H G G H R Q H H Q T F E H V L R A S V -  
 c L T E V I A S I I K P Q N T Y C V R R Y -

ATGCCGTGGTCCAGAACGCGCGCCATGGGCAAGTCCGCAAGGCGCTTCAGAGGCCAGTCT  
 2281 -----+-----+-----+-----+-----+ 2340  
 TACCGCACCAGGTCTTCCGGCGGGTACCCGTGCAGGGGTTCGGAAGTTCCTGGTGCAGA

a M P W S R R P P M G T S A R P S R A T S -  
 b C R G P E G R P W A R P Q G L Q E P R L -  
 c A V V Q K A A H G H V R K A F K S H V S

CTACCTTGACAGAGCTCCAGCCGTACATGCCACAGTTCTGTGGCTCACTGCAGGANAACA  
 2341 -----+-----+-----+-----+-----+ 2400  
 GATGGAACTGTCTGGAGGTCCGGCATGTACCGTGTCAAGCACCGAGTGACCGTCTTNTGT

a L P \* Q T S S R T C D S S W L T C R ? T -  
 b Y L D R P P A V H A T V R G S P A G ? Q -  
 c T L T D L Q P Y M R Q F V A H L Q ? N S -

GCCTCCCTCAGGATCCCGTGTGATGAGCAGAGCTCTCCCTGAATGAGGCCAGCAATG  
 2401 -----+-----+-----+-----+-----+ 2460  
 CGGGCGACTCCCTACGGCAGCAGTAGCTCGTCTCGAAGAGGCACTTACTCCGGTCTGTAC

a A R \* G M P S S S S R A P P \* M R P A V -  
 b P A E G C R R H R A E L L P E \* G Q Q W -  
 c P L R D A V V I E Q S S S L N E A S S G -

GCCTCTTCACCTCTTCTACGCTTCATGTCCACCAAGCGGTCTGCAACAGGGCAAGT  
 2461 -----+-----+-----+-----+-----+ 2520  
 CGGAGAGCTGCAGAGGATGCGAAGTACACGGTGGTGGGCAAGGTAGTCCCGCTTCA

a A S S T S S Y A S C A T T P C A S G A S -  
 b P L R R L P T L H V P P R R A H Q G Q V -  
 c L F D V F L R F M C H H A V R I R G K S -

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Figure 1 is a 10x10 grid of bar charts. The rows represent age groups (18-24, 25-34, 35-44, 45-54, 55-64, 65-74, 75-84, 85-94, 95-104, 105-114) and the columns represent genders (Male, Female). Each bar chart shows the percentage of respondents for each gender within that age group. The data is as follows:

Age Group	Male (%)	Female (%)
18-24	50.0	50.0
25-34	50.0	50.0
35-44	50.0	50.0
45-54	50.0	50.0
55-64	50.0	50.0
65-74	50.0	50.0
75-84	50.0	50.0
85-94	50.0	50.0
95-104	50.0	50.0
105-114	50.0	50.0

[illegible]

A P T S S A R G S R R A F S S P R C S A A -  
 B L R P V P G D P A G L H T I H A A L Q F -  
 C Y V Q C Q C I P Q G S I L S T L L C S L -

-----+-----+-----+-----+-----+-----  
ACAGGATGTCCGCTGTACTCTTTTTCGCACAACGCCCGCCTTGCCCCGACGGG

5 C A T A T W K T S C L R C F G S T G C S -  
6 V L R R H G E Q A V C G D S A G R A A F -  
7 C Y G D M E N K L F A G I R E D G L L L -

2641 +-----+-----+-----+-----+-----+-----+-----+-----+ 2700  
AAGCAAAACCCTACTAAAGAACACACCACATGTGGAGTGGAGTGGGTCCTTTTGGAGC;

a C V W W M I S C W \* H L T S P T R K P S -  
b A F G G \* F I V G D T S P H F R E N L P -  
c R L V D D F L L V T P H L T H A K T F L -

AGTCTGCGACCAAGGCCTCCACAGGGACTTCATACCAGCGCACCACTTCAAAGCCTTCCTGTC

A S C P W S E V S L S M A A W \* T C G R Q -  
 B Q D P G P R C P \* V W I R G E L A E D S -  
 C F T L V R G V P E Y G C V V N L R K T V -

[illegible]

W \* T S L \* K T R P W V A K L L F R C R  
G E L P C R R R C P C W H C F C S D A G -  
V N F P V E D E A L G G T A F V O M F A -

2871 -----+-----+-----+-----+-----+-----+-----+ 2680  
GGGTGCGGATAAGGGACCAAGCCCGACGACGACCCTATGGGCCCTGGACCTGCACCTT

S P T A Y S P G A A C C W I P G P W R C R -  
 D P R P I P L V R P A A G Y P D P G G A E -  
 C H G L F P W C G L L L C T R T L E V O S -

CGCTGATGAGGTGGATACGGGCGCTGGAGGTAGTCTTCGGTCAGAGTGGGAAGTTGGCCGTGA

A T T P A M P G P P S E P V S P S T A A -  
R L L Q L C F D L H Q S Q S H L Q P R L -  
D Y S S Y A R T S I R A S L T E N R G F -

FIGURE 51 (cont.)

TCAGGCTGGGAGGAACATGCTGCAAACTCTTTGGGGTCTTGGGGCTGAAAGTGCACA  
 2941 ----- 3000  
 AGTTGAGACCTCTCTGTACGAGCGTTTBAGAAACCCAGAACGCGACTTCACAGTGT  
  
 S E L G G T C V A N S L G S C G \* S V T  
 Q G W E E H A S Q T L W G L A A E V S Q  
 K A G R N M R R K L F G V L R L K C H S -  
  
 GCCTGTTTCTGCAATTTCCAGCTGAACAGCCTCCAGACGGTGTCCACCAACATCTACAGA  
 3001 ----- 3060  
 CGGACAPAGACCTTAACGTCACACTGTGTCGGAGGTCTGTCACACGTGGTGTAGATGTTCT  
  
 A C F W I C R \* T A S R R C A F T S T R -  
 P V S C F A G E Q P P D G V H Q H L Q D -  
 L F L D L Q V N S L Q T V C T N I Y K T -  
  
 TCTCTTCTGCTCCAGGGTACAGGTTTCACGCATGTGTGCTGAGCTCCCATTTTCATCAGC  
 3061 ----- 3120  
 AGGAGGACGACGCTCCCATGTCCAAAGTGGGTACACACGACCTGAGGGTAAAGTAGTTC  
  
 S S C C R R T G F T H V C C S S H F I S -  
 P F A A G V Q V S R M C A A A P I S S A -  
 L L L Q A Y R F H A C V L Q L P F H O O -  
  
 AAGTTTGGAGAACCCACATTTTCTGCGGTCAATCTCTACACGGCCCTCCCTCTGCT  
 3121 ----- 3180  
 TTCAAACCTTCTTGGGGTGTAAAAAGCACCCGCACTACAGACTCTGCCGGAGCGACACCA  
  
 K F G R T P H F S C A S S L T R P F S A -  
 S L E E P H I F P A R H L \* H G L P L L  
 V W K N P T F F L R V I S D T A S L C Y  
  
 ACTCCATCTCTGAAAGCCAAACAACGCAAGGATGTGCTGGGGGCCAAGGGGGGCCCCCCCC  
 3181 ----- 3240  
 TGAGGTAGGACTTTCGGTCTCTTCCGTCCCTACACCGACCCCGGTTCCCGCCCCCCCCCG  
  
 T P S \* K F R T Q G C R W G P R A F P A -  
 L H F E S Q E R R D V A G G Q G R R R P -  
 S I L K A K N A C M S L C A K C A A C F -  
  
 CTCTGCTCTGGAGGCGGTGCACTGGCTGTGCCACCAAGCATTCCTGCTCAAGCTGACTC  
 3241 ----- 3300  
 GAGACGGGAGGCTTCGGCAGCTCACCCACACCGTGGTTCCTAAGGACAGTTCGACTTAG  
  
 L C P P R P C S G C A T E H S C S S \* L -  
 S A L R G R A V A V P P S I P A Q A D S -  
 L P S E A V Q W L C H Q A F L L K L T R -  
  
 GACACCGTGTACCTAGCTGCTACTCTGGGGTCACTAGGACAGCCAGACCGAGCTGA  
 3301 ----- 3360  
 CTCTGGCACAGTGGATCCACCGTGAAGACCCCACTGAGTCTCTGCGCTCTGGGTGACT  
  
 D T V S P T C H S W G H S G Q F R R S \* -  
 T P C H L R A T P G V T Q D S P D A A E -  
 H R V T Y V F L L G S L R T A Q T Q I S -

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# FIGURE 51 (cont.)

3341 GTGGGAAGCTCCCGG3GAAGACGCTGACTGCGCTGGAG3CGGACGCCAACCCCGACCTGCT  
 ----- 3420  
 CAGCCCTTCGAGGGGCGCCCTGCTGCGACTGACGGGACCTCCGCGCTCGGCTCGGCGCTGACG  
  
 a V G S S R G R R \* L F W R P Q F T R H C -  
 b E E A P G D D A D C P G G R S Q P G T A -  
 c R K L F G T T L T A L E A A A N P A L P -  
  
 3421 CCTCAGACTTCAGAGCCATCCGACTGATG3CCACCCGCGCCACAGCCAGGCGAGAGCA  
 ----- 3480  
 GGAGTCTGAAGTTCTGCTAGGACCTGACTACCGGTGGGCGGCTGCTCGCTCCGCTCTCTCT  
  
 a P Q T S R P S W T D G H P P T A R P R A -  
 b L R L Q D H P G L M A T E P Q T G R E Q -  
 c S D F K T I L D \* W P P A H S Q A E S R -  
  
 3481 GACACCAGCAGCCCTCTCAAGCCCG3CTCTACGTCCTAGGGAGGGAGGGGGCGCCACAC  
 ----- 3540  
 CTGTGCTGCTGCGGACACTCGGCGCCGAGATGACGGGTCCCTCCCTCCCGCGGGGTGTG  
  
 a D T S S F V T P G S T S Q G G R G G P H -  
 b T P A A L S R R A L K P R E G G A A H T -  
 c H Q Q P C H A G L Y V P G R E G E P T T -  
  
 3541 CCAGGCCCGCACCGCTCGGACTCTCAAGCCCTGAGTGAAGTTTGGCGAGGCGCTGCAATG  
 ----- 3600  
 GGTTCGGGGCTGGCGACCTCAGACTTCG3ACTCACTCACAACCGGCTCGGAGCTACA  
  
 a P G P H R W E S E A \* V S V W P R P A C -  
 b Q A R T A G S L R P E \* V P G R G L H V -  
 c K P A P L G V \* G L S E C L A E A C M S -  
  
 3601 CCGGCTGAAG3CTGAGTGTCTCGGCTGAGGCCGAGCGAGTCTCCACCCAACCGCTGAGT  
 ----- 3660  
 GGCGGACTTCCGACTTCAGAGCCCGACTCCGGACTCGCTCAGAGTGGTTCCCGACTCAC  
  
 a P A E G \* V S G \* G L S E C P A K C \* V -  
 b R L F A E C P A E A \* A S V Q P R A E C -  
 c G \* R L S V R L R P E R V S S Q G L S V -  
  
 3661 TCCAGTACACCTGCGCTCTTCACTTCCCGACAGGCTG3CGCTCGGCTCCACCCAGGGCT  
 ----- 3720  
 AGGTGCTGTGACGGCAGAGCTGAACCGCTGTCCGACCGGAGCGGAGGTGGGTCCCG  
  
 a S S T P A V F T S P Q A G A R L H P R A -  
 b P A H L P S S L P H R L A L G S T P G P -  
 c Q H T C R L H F P T G W R S A P P Q G Q -  
  
 3721 AGCTTTTCTCACCAGCAGCCCGGCTTCCACTCCCGACATAGGAATAGTTCATCCCGAGA  
 ----- 3780  
 TCGAANVSGAGTGTCTCGGCGCGAGGTGAGGGGIGTATCCCTTATCAGCTACCGCTCT  
  
 a S F S S P G A R L P L P T \* E \* S T P E  
 b A P P H Q E F G F H S P H R N S P S P D -  
 c L F L T R S P A S T P H I G I V H F Q T -

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[illegible]

A F A I V H P S P C P P L P S T P T I Q V -  
 B S E L F T P R P A L L C L P P P F S R W -  
 C R H C S P L A L P S F A F H P H H P G G

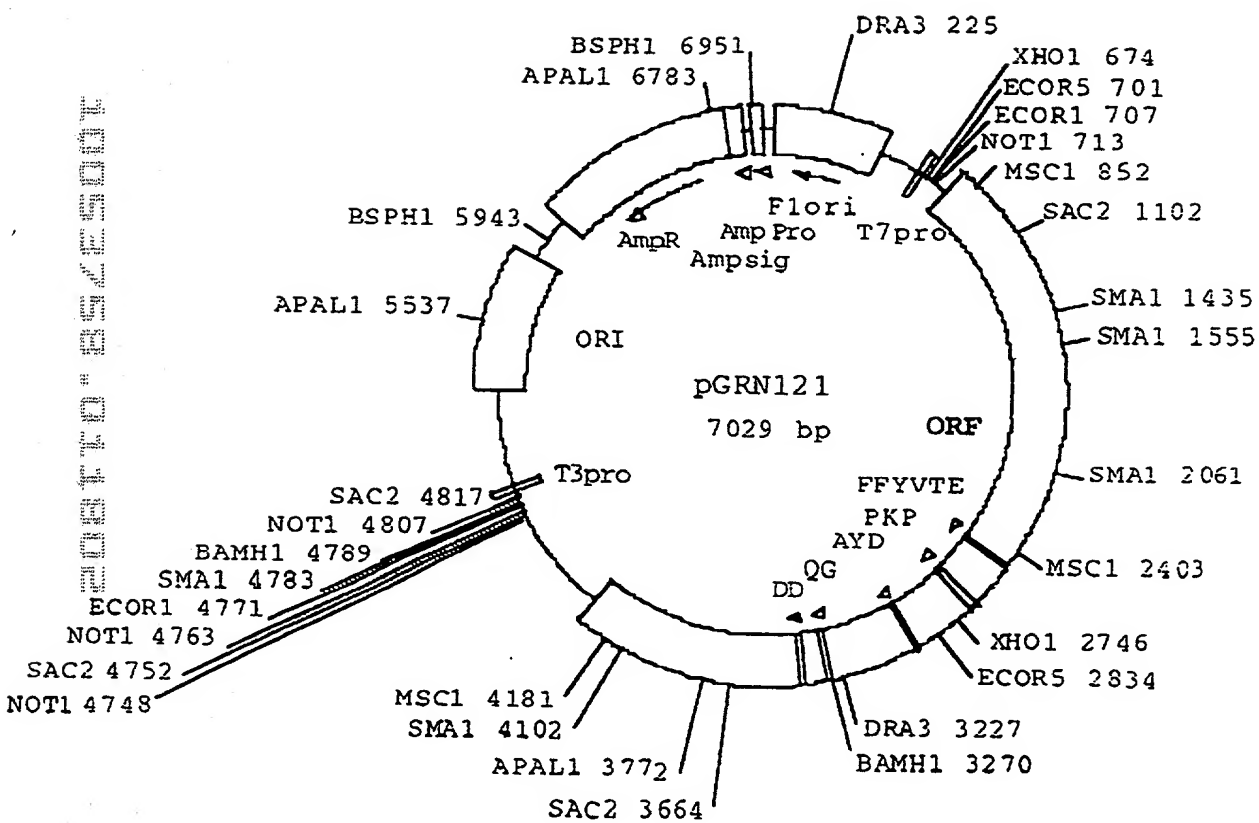
A E T L E R S T L G A L G I W S D Q R C A L -  
 B F F \* E G P W E L W E F G V T K G V P C -  
 C D P E K D F G S S C N L E \* P K V C E V -

A Y T G E D P A P G W G S L W V K L G G C -  
B T O A R T L H L D G G P C G S N W G R V -  
C H R R C P C T W M C V P V G Q I G G E C

A V G V K Y \* I Y E F F S F E K K K K K  
L W E \* N T E Y M S F S V L K K K K K K  
C G S K I L N I \* V F Q F \* K K K K K K -

a	K	K	K	-	
b		K	K	-	
c			K	K	-

FIGURE 52



[illegible]

1  
met  
GCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGCG ATG

10  
pro arg ala pro arg cys arg ala val arg ser leu leu arg ser  
CCG CGC GCT CCC CGC TGC CGA GCC GTG CGC TCC CTG CTG CGC AGC

20 30  
his tyr arg glu val leu pro leu ala thr phe val arg arg leu  
CAC TAC CGC GAG GTG CTG CCG CTG GCC ACG TTC GTG CGG CGC CTG

40  
gly pro gln gly trp arg leu val gln arg gly asp pro ala ala  
GGG CCC CAG GGC TGG CGG CTG GTG CAG CGC GGG GAC CCG GCG GCT

50 60  
phe arg ala leu val ala gln cys leu val cys val pro trp asp  
TTC CGC GCG CTG GTG GCC CAG TGC CTG GTG TGC GTG CCC TGG GAC

70  
ala arg pro pro pro ala ala pro ser phe arg gln val ser cys  
GCA CGG CCG CCC CCC GCC GCC CCC TCC TTC CGC CAG GTG TCC TGC

80 90  
leu lys glu leu val ala arg val leu gln arg leu cys glu arg  
CTG AAG GAG CTG GTG GCC CGA GTG CTG CAG AGG CTG TGC GAG CGC

100  
gly ala lys asn val leu ala phe gly phe ala leu leu asp gly  
GGC GCG AAG AAC GTG CTG GCC TTC GGC TTC GCG CTG CTG GAC GGG

110 120  
ala arg gly gly pro pro glu ala phe thr thr ser val arg ser  
GCC CGC GGG GGC CCC CCC GAG GCC TTC ACC ACC AGC GTG CGC AGC  
↑

130  
tyr leu pro asn thr val thr asp ala leu arg gly ser gly ala  
TAC CTG CCC AAC ACG GTG ACC GAC GCA CTG CGG GGG AGC GGG GCG

FIGURE 53 (cont.)

				140											150
trp	gly	leu	leu	leu	arg	arg	val	gly	asp	asp	val	leu	val	his	
TGG	GGG	CTG	CTG	CTG	CGC	CGC	GTG	GGC	GAC	GAC	GTG	CTG	GTT	CAC	
								160							
leu	leu	ala	arg	cys	ala	leu	phe	val	leu	val	ala	pro	ser	cys	
CTG	CTG	GCA	CGC	TGC	GCG	CTC	TTT	GTG	CTG	GTG	GCT	CCC	AGC	TGC	
				170											180
ala	tyr	gln	val	cys	gly	pro	pro	leu	tyr	gln	leu	gly	ala	ala	
GCC	TAC	CAG	GTG	TGC	GGG	CCG	CCG	CTG	TAC	CAG	CTC	GGC	GCT	GCC	
								190							
thr	gln	ala	arg	pro	pro	pro	his	ala	ser	gly	pro	arg	arg	arg	
ACT	CAG	GCC	CGG	CCC	CCG	CCA	CAC	GCT	AGT	GGA	CCC	CGA	AGG	CGT	
				200											210
leu	gly	cys	glu	arg	ala	trp	asn	his	ser	val	arg	glu	ala	gly	
CTG	GGA	TGC	GAA	CGG	GCC	TGG	AAC	CAT	AGC	GTC	AGG	GAG	GCC	GGG	
								220							
val	pro	leu	gly	leu	pro	ala	pro	gly	ala	arg	arg	arg	gly	gly	
GTC	CCC	CTG	GGC	CTG	CCA	GCC	CCG	GGT	GCG	AGG	AGG	CGC	GGG	GGC	
				230											240
ser	ala	ser	arg	ser	leu	pro	leu	pro	lys	arg	pro	arg	arg	gly	
AGT	GCC	AGC	CGA	AGT	CTG	CCG	TTG	CCC	AAG	AGG	CCC	AGG	CGT	GGC	
								250							
ala	ala	pro	glu	pro	glu	arg	thr	pro	val	gly	gln	gly	ser	trp	
GCT	GCC	CCT	GAG	CCG	GAG	CGG	ACG	CCC	GTT	GGG	CAG	GGG	TCC	TGG	
				260											270
ala	his	pro	gly	arg	thr	arg	gly	pro	ser	asp	arg	gly	phe	cys	
GCC	CAC	CCG	GGC	AGG	ACG	CGT	GGA	CCG	AGT	GAC	CGT	GGT	TTC	TGT	
								280							
val	val	ser	pro	ala	arg	pro	ala	glu	glu	ala	thr	ser	leu	glu	
GTG	GTG	TCA	CCT	GCC	AGA	CCC	GCC	GAA	GAA	GCC	ACC	TCT	TTG	GAG	

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Figure 1 displays 12 histograms arranged in a 6x2 grid, showing the distribution of the number of non-zero elements in the vector  $x$  for different values of  $n$ . The left column shows distributions for  $n = 10, 20, 30, 40, 50, 60$ , and the right column shows distributions for  $n = 70, 80, 90, 100, 110, 120$ . Each histogram has 'Number of non-zero elements' on the x-axis and 'Frequency' on the y-axis. The distributions are roughly bell-shaped and centered around  $n/2$ .

290 300  
gly ala leu ser gly thr arg his ser his pro ser val gly arg  
GGT GCG CTC TCT GGC ACG CGC CAC TCC CAC CCA TCC GTG GGC CGC

310  
gln his his ala gly pro pro ser thr ser arg pro pro arg pro  
CAG CAC CAC GCG GGC CCC CCA TCC ACA TCG CGG CCA CCA CGT CCC

320 330  
trp asp thr pro cys pro pro val tyr ala glu thr lys his phe  
TGG GAC ACG CCT TGT CCC CCG GTG TAC GCC GAG ACC AAG CAC TTC

340  
leu tyr ser ser gly asp lys glu gln leu arg pro ser phe leu  
CTC TAC TCC TCA GGC GAC AAG GAG CAG CTG CGG CCC TCC TTC CTA

350 360  
leu ser ser leu arg pro ser leu thr gly ala arg arg leu val  
CTC AGC TCT CTG AGG CCC AGC CTG ACT GGC GCT CGG AGG CTC GTG

370  
glu thr ile phe leu gly ser arg pro trp met pro gly thr pro  
GAG ACC ATC TTT CTG GGT TCC AGG CCC TGG ATG CCA GGG ACT CCC

380 390  
arg arg leu pro arg leu pro gln arg tyr trp gln met arg pro  
CGC AGG TTG CCC CGC CTG CCC CAG CGC TAC TGG CAA ATG CGG CCC

400  
leu phe leu glu leu leu gly asn his ala gln cys pro tyr gly  
CTG TTT CTG GAG CTG CTT GGG AAC CAC GCG CAG TGC CCC TAC GGG

410 420  
val leu leu lys thr his cys pro leu arg ala ala val thr pro  
GTG CTC CTC AAG ACG CAC TGC CCG CTG CGA GCT GCG GTC ACC CCA

430  
ala ala gly val cys ala arg glu lys pro gln gly ser val ala  
GCA GCC GGT GTC TGT GCC CGG GAG AAG CCC CAG GGC TCT GTG GCG

FIGURE 53 (cont.)

440  
ala pro glu glu glu asp thr asp pro arg arg leu val gln leu  
GCC CCC GAG GAG GAG GAC ACA GAC CCC CGT CGC CTG GTG CAG CTG

460  
leu arg gln his ser ser pro trp gln val tyr gly phe val arg  
CTC CGC CAG CAC AGC AGC CCC TGG CAG GTG TAC GGC TTC GTG CGG

470  
ala cys leu arg arg leu val pro pro gly leu trp gly ser arg  
GCC TGC CTG CGC CGG CTG GTG CCC CCA GGC CTC TGG GGC TCC AGG

490  
his asn glu arg arg phe leu arg asn thr lys lys phe ile ser  
CAC AAC GAA CGC CGC TTC CTC AGG AAC ACC AAG AAG TTC ATC TCC

500  
leu gly lys his ala lys leu ser leu gln glu leu thr trp lys  
CTG GGG AAG CAT GCC AAG CTC TCG CTG CAG GAG CTG ACC TGG AAG

520  
met ser val arg asp cys ala trp leu arg arg ser pro gly val  
ATG AGC GTG CGG GAC TGC GCT TGG CTG CGC AGG AGC CCA GGG GTT

530  
gly cys val pro ala ala glu his arg leu arg glu glu ile leu  
GGC TGT GTT CCG GCC GCA GAG CAC CGT CTG CGT GAG GAG ATC CTG

550  
ala lys phe leu his trp leu met ser val tyr val val glu leu  
GCC AAG TTC CTG CAC TGG CTG ATG AGT GTG TAC GTC GTC GAG CTG

560  
leu arg ser phe phe tyr val thr glu thr thr phe gln lys asn  
CTC AGG TCT TTC TTT TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC

580  
arg leu phe phe tyr arg pro ser val trp ser lys leu gln ser  
AGG CTC TTT TTC TAC CGG CCG AGT GTC TGG AGC AAG TTG CAA AGC

590  
ile gly ile arg gln his leu lys arg val gln leu arg glu leu  
ATT GGA ATC AGA CAG CAC TTG AAG AGG GTG CAG CTG CGG GAG CTG

FIGURE 53 (cont.)

610  
ser glu ala glu val arg gln his arg glu ala arg pro ala leu  
TCG GAA GCA GAG GTC AGG CAG CAT CGG GAA GCC AGG CCC GCC CTG

620 630  
leu thr ser arg leu arg phe ile pro lys pro asp gly leu arg  
CTG ACG TCC AGA CTC CGC TTC ATC CCC AAG CCT GAC GGG CTG CGG

640  
pro ile val asn met asp tyr val val gly ala arg thr phe arg  
CCG ATT GTG AAC ATG GAC TAC GTC GTG GGA GCC AGA ACG TTC CGC

650 660  
arg glu lys arg ala glu arg leu thr ser arg val lys ala leu  
AGA GAA AAG AGG GCC GAG CGT CTC ACC TCG AGG GTG AAG GCA CTG

670  
phe ser val leu asn tyr glu arg ala arg arg pro gly leu leu  
TTC AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC GGC CTC CTG

680 690  
gly ala ser val leu gly leu asp asp ile his arg ala trp arg  
GGC GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC TGG CGC

700  
thr phe val leu arg val arg ala gln asp pro pro pro glu leu  
ACC TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG CTG

710 720  
tyr phe val lys val asp val thr gly ala tyr asp thr ile pro  
TAC TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC

730  
gln asp arg leu thr glu val ile ala ser ile ile lys pro gln  
CAG GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG

740 750  
asn thr tyr cys val arg arg tyr ala val val gln lys ala ala  
AAC ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC

760  
his gly his val arg lys ala phe lys ser his val ser thr leu  
CAT GGG CAC GTC CGC AAG GCC TTC AAG AGC CAC GTC TCT ACC TTG

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FIGURE 53 (cont.)

770 780  
thr asp leu gln pro tyr met arg gln phe val ala his leu gln  
ACA GAC CTC CAG CCG TAC ATG CGA CAG TTC GTG GCT CAC CTG CAG

790  
glu thr ser pro leu arg asp ala val val ile glu gln ser ser  
GAG ACC AGC CCG CTG AGG GAT GCC GTC GTC ATC GAG CAG AGC TCC

800 810  
ser leu asn glu ala ser ser gly leu phe asp val phe leu arg  
TCC CTG AAT GAG GCC AGC AGT GGC CTC TTC GAC GTC TTC CTA CGC

820  
phe met cys his his ala val arg ile arg gly lys ser tyr val  
TTC ATG TGC CAC CAC GCC GTG CGC ATC AGG GGC AAG TCC TAC GTC

830 840  
gln cys gln gly ile pro gln gly ser ile leu ser thr leu leu  
CAG TGC CAG GGG ATC CCG CAG GGC TCC ATC CTC TCC ACG CTG CTC

850  
cys ser leu cys tyr gly asp met glu asn lys leu phe ala gly  
TGC AGC CTG TGC TAC GGC GAC ATG GAG AAC AAG CTG TTT GCG GGG

860 870  
ile arg arg asp gly leu leu leu arg leu val asp asp phe leu  
ATT CGG CGG GAC GGG CTG CTC CTG CGT TTG GTG GAT GAT TTC TTG

880  
leu val thr pro his leu thr his ala lys thr phe leu arg thr  
TTG GTG ACA CCT CAC CTC ACC CAC GCG AAA ACC TTC CTC AGG ACC

890 900  
leu val arg gly val pro glu tyr gly cys val val asn leu arg  
CTG GTC CGA GGT GTC CCT GAG TAT GGC TGC GTG GTG AAC TTG CGG

910  
lys thr val val asn phe pro val glu asp glu ala leu gly gly  
AAG ACA GTG GTG AAC TTC CCT GTA GAA GAC GAG GCC CTG GGT GGC

920 930  
thr ala phe val gln met pro ala his gly leu phe pro trp cys  
ACG GCT TTT GTT CAG ATG CCG GCC CAC GGC CTA TTC CCC TGG TGC



FIGURE 53 (cont.)

940  
gly leu leu leu asp thr arg thr leu glu val gln ser asp tyr  
GGC CTG CTG CTG GAT ACC CGG ACC CTG GAG GTG CAG AGC GAC TAC

950 960  
ser ser tyr ala arg thr ser ile arg ala ser val thr phe asn  
TCC AGC TAT GCC CGG ACC TCC ATC AGA GCC AGT GTC ACC TTC AAC

970  
arg gly phe lys ala gly arg asn met arg arg lys leu phe gly  
CGC GGC TTC AAG GCT GGG AGG AAC ATG CGT CGC AAA CTC TTT GGG

980 990  
val leu arg leu lys cys his ser leu phe leu asp leu gln val  
GTC TTG CGG CTG AAG TGT CAC AGC CTG TTT CTG GAT TTG CAG GTG

1000  
asn ser leu gln thr val cys thr asn ile tyr lys ile leu leu  
AAC AGC CTC CAG ACG GTG TGC ACC AAC ATC TAC AAG ATC CTC CTG

1010 1020  
leu gln ala tyr arg phe his ala cys val leu gln leu pro phe  
CTG CAG GCG TAC AGG TTT CAC GCA TGT GTG CTG CAG CTC CCA TTT

1030  
his gln gln val trp lys asn pro thr phe phe leu arg val ile  
CAT CAG CAA GTT TGG AAG AAC CCC ACA TTT TTC CTG CGC GTC ATC

1040 1050  
ser asp thr ala ser leu cys tyr ser ile leu lys ala lys asn  
TCT GAC ACG GCC TCC CTC TGC TAC TCC ATC CTG AAA GCC AAG AAC

1060  
ala gly met ser leu gly ala lys gly ala ala gly pro leu pro  
GCA GGG ATG TCG CTG GGG GCC AAG GGC GCC GCC GGC CCT CTG CCC

1070 1080  
ser glu ala val gln trp leu cys his gln ala phe leu leu lys  
TCC GAG GCC GTG CAG TGG CTG TGC CAC CAA GCA TTC CTG CTC AAG

1090  
leu thr arg his arg val thr tyr val pro leu leu gly ser leu  
CTG ACT CGA CAC CGT GTC ACC TAC GTG CCA CTC CTG GGC TCA CTC

FIGURE 53 (cont.)

1100 1110  
arg thr ala gln thr gln leu ser arg lys leu pro gly thr thr  
AGG ACA GCC CAG ACG CAG CTG AGT CGG AAG CTC CCG GGG ACG ACG

1120  
leu thr ala leu glu ala ala ala asn pro ala leu pro ser asp  
CTG ACT GCC CTG GAG GCC GCA GCC AAC CCG GCA CTG CCC TCA GAC

1130 1132  
phe lys thr ile leu asp OP  
TTC AAG ACC ATC CTG GAC TGA TGGCCACCCGCCACAGCCAGGCCGAGAGCAGA  
CACCAGCAGCCCTGTCACGCCGGGCTCTACGTCCCAGGGAGGGAGGGGCGGCCACACCC  
AGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGAGTGTTTGGCCGAGGCCTGCATGTCC  
GGCTGAAGGCTGAGTGTCGGCTGAGGCCTGAGCGAGTGTCAGCCAAGGGCTGAGTGTC  
CAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCAGGGCCAG  
CTTTTCYTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCCCCAGATT  
CGCCATTGTTACCCYTCGCCCTGCCYTCTTTGCCTTCCACCCCCACCATCCAGGTGGA  
GACCCTGAGAAGGACCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGTGCCCTGTA  
CACAGGCGAGGACCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGGGGAGGTGC  
TGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTTGRAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAA

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**FIGURE 54**

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